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May 25, 2003, 08:48:53 ; Search time 2746 Seconds (without alignments) 10958.595 Million cell updates/sec US-09-955-526-3 1034 1 gagcaaacataacattgtct.....ataaggaaagttccttgtga 1034 4109280 Total number of hits satisfying chosen parameters: 2054640 segs, 14551402878 residues Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries OM nucleic - nucleic search, using sw model IDENTITY NUC Gapop 10.0 , Gapext 1.0 11. 9D ba:*
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Pred. No. is the number of results predicted by chance to have a

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Direct Submission

Submitted (11-MaR-2002) Ceres, Inc, 3007 Malibu Caryon Road, Malibu, CA 90265, USA

This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with Known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the certain all end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or Laker cotypes and therefore may contain polymorphisms when compaced to sequences from COl-0. Genset carried out the library production and sequencing of the full-length clones. Geres, Inc. carried out the clustering of the full-length clones. Geres, Inc. carried out the clustering of the full-length clones. Geres, Inc. carried out the clustering of the corganism="Arabidopsis thaliana" (AD znef="taxon:3702" clones; and sequence assembly.

| Clones | Companism="harabidopsis thaliana" | AD znef="taxon:3702" clones | AD z
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NLQFASSIFGGSASIFKFELYFGLLIFVGYWVVDTQEIIEKAHLGDWDYVXHSLTEF
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 1066)
I (bases 1 to 1066)
Feldmann, K.A., Flavell, R.B., White,O. and Salzberg, S.L.
Feldmann, K.A., Flavell, R.B., White,O. and Salzberg, S.L.
Full-length messenger RNA sequences greatly improve genome
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( Cases 1 to 1066)

Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. Feldmann, K.

Full-Length cDNA from Arabidopsis thaliana
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3 toases 1 to 1066)
Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. Feldmann, K.
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Unpublished

(bases 1 to 1293)

Bolduc,N., Pitre,F. and Brisson,L.,

Direct Submission
Submitted (11-707-2001) Biochemistry and Microbiology, Laval
University, Quebec GIK 7P4, Canada
Location/Qualifiers

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                         Score 428.8; DB 8;
Pred. No. 1.6e-103;
0; Mismatches 197;
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                         Query Match
Best Local Similarity 73.73
Matches 560; Conservative
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Rosidae, eurosids II; Brassicales; Brasslcaceae; Arabidopsis:

VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

(bases 1 to 994)

REFERENCE

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The search of the 
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Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Dong, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C., Toriumi, M., Wh.H.C., Yamamura, Y., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin, Neumann, G., Kawai, J., Xim, C., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Sakusai, K., Davis, R.W., Ecker, J.R., and Theologis, A., Arabidopais Full Length cDNA Clones
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41.3%; Score 427.2; DB 8;
Best Local Similarity 73.6%; Pred. No. 4.4e-103;
Matches 559; Conservative 0; Mismatches 198;
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/db.sucf="traxon:3702"

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/note="challenged with Pseudomonas syringae pv. tomato 491 388 gaccicaaccarcriraticacricatriferragaacricicariaccririferriritica 447 551 507 611 567 671 568 AICTTTAAGTTTGAGTTGTACTTTGGACTTTTGATCTTTGTGGGAIACATGGTGGTGGAC 627 311 TACCICCATGIGCITCIGGALIATCGGCGGTATTCTTACAACGATTGGATGTATTGGAACT 267 AIGGIGIGGITCICICAGCICCICCITAICAAGAGCAAAAAAGGGTGGCICTICIGAIG 371 GCAGCTGCACTTTTGAAGGCGCCTCTATTGGTCCTCTGATTGAGCTGGCATTAACTTC 431 ererciecrericineaaderecricieriesececerraareaagreecaarieareir 387 191 147 251 207 72 AAGAAGAAGAAGAATGGAAGGTTTCACATGGTTCTTCGACTCGCAATCTGCCTCTCGC 131 pathogen challenge Unpublished 2 (bases 1 to 1006) Sanchez,P., de Torres Zabala,M. and Grant,M. Direct Submission Submitted (24-NOV-1999) Biological Sciences, Wye College, Mye, Ashford, Kent TN25 5.4H, UK Gaps 87 GCTGCTGCCATGTTGGCAAGGCGCAGGAAGTACTTGTACCTCGGGGGCCTTCTTTCATCT 508 GGCTTGTCTATGCTAATGTGGCTCCAGTTTGCCTCTTCAATCTTTGGTGGCTCTGCATCT 612 GITTICAACTITGAGTIGTATTTTGGACTCTTGGTGTTTGTGGGCTTACATCGTCTTTGAC 552 GOCGICTCCCTTCTCGTTGCACTTTGCATCCTCCATTTTTGGTGGTTCCATGGCT AACCGCTGGAGTTATGATTCTCTCAAAAACTTCCGCCAGATCTCACCTCTCGTTCAAACT TACCTTCACATTCTATGGAATATCGGTGGCCTCCTCACAACAATGGCTTGCATGGGAAGC 31 AAAAAAAACGAACCAATGGATGCGTTCTTCCTTCTTCGATTCTCAACCTG---GTAGC CATCTCAAGCAGGTGTACCTTACGCTATGCTGTGCTTTAGTGGCATCGGCTGCTGGGGCT 148 CATCITAAACGGGITTATITGACCTIAIGITGTGCTCTTGTGGCGTCTGCGTTTGGAGCT GATCCAAGCATTGTGTTTGGCGCTTTTGTAGGTTGTGCTTGTGGTTTTTTGGTTGCTTCTCA т .. Length 1006; Indels Query Match
41.3%; Score 427.2; DB 8;
Best Local Similarity 73.6%; Pred. No. 4.4e-103;
Matches 559; Conservative 0; Mismatches 198; /product="Bax inhibitor 1" /protein_id="AAG35727.1" /db_xref="GI:11493975" DC3000::avrRPM1" 46. .789 /note="AtBI-1" /codon_start=1 1006 source BASE COUNT ORIGIN 132 88 252 208 312 268 372 328 432 492 JOURNAL REFERENCE AUTHORS TITLE JOURNAL 192 CDS FEATURES g g ò g ò g 8 원 8 임 Š g ò a à g 8 ð ઠે

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/product="Bax inhibitor-1"
/product="Bax inhibitor-1"
/protein id="BAA89541.2"
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WLQFASSIFGGSASIFKEELYFGLLIFVGYMVVDTQEIIEKAHLGDMDYVKHSITLEFT
DFVAVFVRILIIMLKNSADKEEKKKKRRN"
                                                                                                                                                                                                                  AB025927 1117 bp mRNA linear PLN 04-MAR-2000
Arabidopsis thaliana AtBI-1 mRNA for Bax inhibitor-1, complete cds.
AB025927
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Kawai,M. and Uchimiya,H.

Direct Submission

Submitted (06-APR-1999) Hirofumi Uchimiya, University of Tokyo,

Inst. Mol. Cellu. Biosci., Cellular Function; 1-1-1 Yayoi,

Bunkuo-ku, Tokyo 113-0032, Japan

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(B-mail:uchimiya@inchns.iam.u-tokyo.ac.jp, Tel:81-3-3812-2910,

Fax:81-3-3812-2910)

On Mar 8, 2000 this sequence version replaced gi:6716123.
                                                                                                                                                                                                                                                                                                                                                                                              Kawai,M., Pan, D., Reed, J.C. and Uchimiya, H.
Evolutionally conserved plant homologue of the Bax inhibitor-1
(Bi-1) gene capable of suppressing Bax-induced cell death in
yeast(1)
20086876
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                            687
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                                                                                    ACCCTITICACTGACTITIGIAGCTGTGTTTTCTCGGATTCTCATGATGTTGAAGAAC 747
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                                                                                                                                                                                                                                                                                         Bax inhibitor-1.
Arabidopsis thaliana (strain:Columbia) cDNA to mRNA.
Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
              ACCCTITICACAGATITIGGCGCTGTTTTGTGCGGATTCTGATCATGTTAAAGAAT
Query Match 41.3%; Score 427.2; DB 8; Length 1117; Best Local Similarity 73.6%; Pred. No. 4.4e-103; Matches 559; Conservative 0; Mismatches 198; Indels 3;
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/strain="Columbia"
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/gene="AtBI-1"
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicacee; Arabidopsis.

I (bases 1 to 775)

Standa,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M.,

Deng,J.M., Goldamith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L.,

Tang,C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L.,

Carninci,P., Cheu,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,

Jones,T., Kamiya,A., Karlin,Neumann,G., Kami,C., Lam,B.,

Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T.,

Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K.,

Arabidopsis Open Reading Frame (ORF) Clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AX114059 775 bp mRNA linear PLN 31-MAY-2002
Arabidopsis thaliana putative Bax inhibitor-1 (At5g47120) mRNA,
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Yamada,K., Dah, Chang,C.H., Chang,E., Dale,J.M.,
Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L.,
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/protein id="AAM$1107.1"
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SVGPLIKVAIDVDPSILITAFVGTAIAFVCFSAAAMIARRREYLYLGGLLSSGLSMLM
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DFVAVFVRILIIMLKNSADKEEKKKKRRN"
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                                                                                                                                             Submitted (16-M2Y-2002) Plant Gene Expression Center, 800 Buchanan Street, Albany, Ca 94710, USA
The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                              The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORP) clones using the RAFL cDNAs: Yamada.K., Banh,J., Chan,M.M., Chang.C.H., Chang.E., Dale,J.M., Deng.J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Chenk,K., Jones,T., Karlin-Neumann,G., Kim,C., Lam,B., Lih,J., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamada,K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally
to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP
/PGEC) contributed equally to this work as PIs.
__iocation/Qualifiers
Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Haysshizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T. Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A., Shinozaki, K., Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Arabidopsis thaliana"
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ecotype: Columbia"
1. .775
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153 c 176
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1010 bp mRNA linear PLN 16-JUL-2001
Brassica napus Bax inhibitor 1 (BI-1) mRNA, complete cds.
AF390555
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Brassica napus

Bukaryota, napus

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,

Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,

Sosidae, eurosida II, Brassicales, Brassicaceae, Brassica.

[ (Dases I to 1010)

Bolduc, N. and Brisson, L.

Characterization of Bax inhibitor I from Brassica napus

Unpublished

2 (bases I to 1010)
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Direct Submission
Submitted (11-JUN-2001) Biochemistry and Microbiology, Laval
University, Quebec GIK 7P4, Canada
Location/Qualifiers
                                                                                                                                                                                                                                       358 ATCACTGCATTTGTTGGAACTGCGATAGCGTTTGTCTGTTTCTCAGCAGCAGCAATGTTA
                                                                                              GAAGGCCCCCCTCTATTGGTCCTCTGATTGAGCTGGGCATTAACTTCGATCCAAGCATTGTG
                                                                                                                                              GAAGGTGCTTCTGTTGGCCCCTTGATCAAGTGGCAATTGATGTTGACCCAAGCATCCTT
                                                                                                                                                                                             TITGGCGCTTTTGTAGGTTGTGCTGTTTTTGGTTGCTTCTCAGCTGCTGCCATGTTG
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/cultivar="Westar"

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.1010
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us-09-955-526-3.rg

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WLQPASSIFGGGSASIFKELYFQGILIFYGYWYVDTQDIIEKAHLGDMDYVKHSLTLFT
DFVAVFVRLIIMLKNSADKEDKKKRRRN" ä 249 541 489 601 549 661 550 crcracarccarcriraagriraagcriciacriridaacricriraarcririgaagaracar 609 721 699 189 301 309 421 481 370 agiricárrirreacceaadcarcercareacrecerririoredaacrecearacerrirar 429 722 GCATGCATTGACCCTTTTCACAGATTTTGGCGCTGTTTTTGTGCGGATTCTGATCATTAT 781 241 361 310 ccricientrerererecretreresaagerecricaertecricerecertareaaneage 369 62 CTCGAAGAAGAAGAAGAAGAACAATGGAAGGTTTCACATCGTTCTTCGACTCGCAATC 121 TGCCTCTCGCAACCGCTGGAGTTATGATTCTCTCAAAACTTCCGCCAGATCTCACCTCT 181 TG---GIAGCAGAAGCTGGAGCTATGATTCTCTCTAAAAACCTCCGTCAGATTTCTCCCCTC 129 Gaps 72 remmearendecencrecenteregaracaerrecarecarecarringereg 490 gerrhearcraderrarecaractrareracerreagriracererrecarerragia CGTCTTTGACACCCCAAGAATTATTGAGAAGGCTCACTTGGGTGATATGGATTACGTTAA 610 GGTGGACACACAAAATATAAAAAAAGGCCCACCTCGGTGACATGGATACGTGAA 670 ACATTOGTTGACCCTTTTCACCGATTTTGTAGCTGTTTTGTTCGTGTTCTCATCATTAT CTTTGGAAGCATTAGCTGCTCTCTCTTCTTATGAACAACAAAGAGCTTTTC 602 TICCATGGCIGITITICAAGITIGAGTIGIATITITGGACTCTIGGIGITITGIGGCTACAT 190 GTTTGGAGCTTACCTCCACGTGCTCTGGAACATAGGTGGTATTCTCACTACCATTGGATG CATGGGAAGCATGGTGGCTTCTCTCTCAGCTCCTTCTATCAAGAGCAAAAAAGGGTGGC 362 TCTTCTGATGGCAGCTGCACTTTTTGAAGGCGCCTCTATTGGTCCTCTGATTGAGCTGGG CATTAACTTCGATCCAAGCATTGTGTTTTGCGCGCTTTTGTAGGTTGTGCTGTGGTTTTTGG TTGCTTCTCAGCTGCTGCCATGTTGGCAAGGCGCAGGGAGTACTTGTACCTCGGGGGCCT CTGTTTCTCAGGGGCAGGATGTTGGCAAGACGCGAGAGAGTACCTCTACCTCGGAGGACT CGTTCAAACTCAACGAGGTGTACCTTACGCTATGCTGTGCTTTAGTGGCATCGGC cerccagaarcarcreaagaggirraarcreacrergrergregercregringegrerec TGCTGGGGCTTACCTTCACATTCTATGGAATATCGGTGGCCTCCTCACAACAATGGCTTG crrahangcahanggahanggacanggarrcantercencencentranggarrenganc ъ, Length 1010; 831 gcrigaagaacricggcagaraaagaagaraaaaagagaggaggaacr 779 40.4%; Score 418; DB 8; Length 1072.3%; Pred. No. 1.3e-100; Live 0; Mismatches 210; Indels GTTAAAGAATGCATCTGAGAAGGAAGAAGAAGAAGAAGAAGAACT 232 g 203 G Conservative Similarity φ. 244 Query Match Best Local Simi Matches 557; BASE COUNT ORIGIN 122 130 250 430 542 662 782 242 302 482 13 73 182 d g 엄 8 d ò à 셤 ò à g ò ò g ò 임 ò g ò 엄 ò d ö a ò

AF453320 1013 bp mRNA linear PLN 27-DEC-2001 Brassica oleracea bax inhibitor-like protein (BII) mRNA, complete cds. GI:17981373 AF453320 AF453320.1 LOCUS ACCESSION VERSION KEYWORDS RESULT 8 AF453320

493

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200 c 233 g 326 t /gene="Bil" /note="may be involved with programmed cell death; similar to Arabidopsis thaliana and Homo sapiens bax inhibitor" ij Brassica oleracea
Bruszycza, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicacea; Brassica.
I (bases 1 to 1013)
I (bases 1 to 1013)
Bason, J.R., Sinclair, B.K., Watson, L.M., Bucknell, T.T. and death 3; Gaps Private Bag AGAAGAAGAACAATGGAAGGTTTCACATGGTTCTTCGACTCGCAATCTGCCTCTCGCA The isolation and characterization of broccoli homologs to Arabidopsis PCD genes, LSD1 and B1: their role during cell DB 8; Length 1013; and senescence Unpublished 2 (bases 1 to 1013) 2 (bases 3, Sinclair, B.K., Watson, L.M., Bucknell, T.T. Eason, J.R. Indels Research, Score 413.4; DB 8; Pred. No. 2.1e-99; 0; Mismatches 206; Direct Submission Submitted (25-NOV-2011) Crop and Food Palmerston North 5301, New Zealand Location/Qualifiers 1. .1013 /organism="Brassica oleracea" /db_xref="taxon:3712" 1. _1013 /gene="BI1" 15. .758 Query Match
Best Local Similarity 72.5%;
Matches 550; Conservative Brassica oleracea source BASE COUNT ORIGIN SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL 73 AUTHORS JOURNAL REFERENCE CDS FEATURES ઠે

417 372 432 312 237 297 357 492 192 117 252 177 552 57 298 TGTCTGCTGTTCTCGAAGGTGCTTCAGTTCGCTTGATCAAGTGGCAGTTGATTTTG ACCECTGGAGTTATGATTCTCTCAAAAACTTCCGCCAGATCTCACCTCTCGTTCAAACTC TGGTGTGGCTTCTCTCTCTCTCTTATCAAGAGCAAAAAGGGTGGCTCTTCTGATGG rdainridicricircrericcricirrargacaacaaaaaaaaacriniccricirric CAGCTGCACTTTTTGAAGGCGCCTCTATTGGTCCTCTGATTGAGCTGGGCATTAACTTCG Acceaagearcereareacrecegrreficegaacrecearagecrrrarerefere CTGCTGCCATGTTGGCAAGGCGCAGGAGTACTTGTACCTCGGGGGGCCTTCTTTCATCTG 1 AGAAAACAAAAGGCATGGATTCATTCTCGTCCTTCGATTCTCAACCTG---GTAGCA 118 ATCTCAAGAGGGGTTTAACTCACTCTGTGTTGTGCTCTCGTTGCGTCTGCGTTTGGAGCTT ACCTTCACATTCTATGGAATATGGGTGGCCTCCTCACAACAATGGCTTGCATGGGAAGCA ATCCAAGCATTGTGTTTGGCGCTTTTGTAGGTTGTGCTGGTTTTTTGGGTTGCTTCTCAG ATCTCAAGCAGGTGTACCTTACGCTATGCTGTGCTTTAGTGGCATCGGCTGCTGGGGCTT 178 238 373 433 358 133 193 253 313 9 8 셤 g ઠે q d ò 임 δ d 셤 ઠે ò ò

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SVGPLIKVAVDFDPSILITAFVGTAIAPICFSGAAMLARRREYLYLGGLLSSGLSMLM
WLQPASSIFGGSASIFKFELYFGLLIFVGYMVVDTQEIIEKAHLGDMDYVKHALTLFT
                                                                                                                                                                                                                                                                                                                                                                                      PLN 27-DEC-2001
mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots; Rosidae, eurosida II, Brassicales, Brassicaceae, Brassica. (bases 1 to 1019)
Coupe, S.A., Sinclair, B.K., Watson, L.M., Bucknell, T.T. and Eason, J.R.
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                                                                                                                                                                                                                                          658 CCCTTTTCACCGATTTTGTAGCTGTGTTTGTTGGTGTTCTCATCATTATGCTGAAGAACT 717
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                                                                                                                                                                                         598 crcaadararraradadadadeccaacercegreacaregarracercaaacarregra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EBOULD. The isolation and characterization of broccoli homologs to Arabidopsis PCD genes, LSDI and BI: their role during cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
2 (bases 1 to 1019)
Coupe,S.A., Sinclair,B.K., Watson,L.M., Bucknell,T.T. and
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Brassica oleracea bax inhibitor-like protein (BI2)
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Submitted (19-NOV-2001) Crop and Food
Palmerston North 5301, New Zealand
Location/Qualifiers
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1. .1019
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AF453321.1 GI:17981375
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54. .794
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Kawai,M., Pan,L., Reed,J.C. and Uchimiya,H.
Evolutionally conserved plant homologue of the Bax inhibitor-1
Evolutionally conserved plant bamologue of the Bax inhibitor-1
yeast(1)
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Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Bax inhibitor-1.
Oryza sativa (strain:Yamahoushi) cDNA to mRNA.
Oryza sativa
Pred. No. 1.3e-95;
0; Mismatches 213;
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CVALAASAYGAYLHVALNIGGMLTMLGCVGSIAWLFSVPVFBERKRFGILLAAALEG
ASVGPLIKLAYDFDSSILVTAFYGTLIFLAFGGTTCAALVAKRRFYLVLGGLLSSGLSIL
IMLQFAASIFGHSTGSPRFEVYFGLIFFGYWVYDTQEIIERAHHGDMDYIKHALTLF
TDFVAVLVRILVIMLKAASDKSEEKKRKKRS"
295 G 307 G 307
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Kawai, M. and Uchimiya, H.

Kawai, M. and Uchimiya, H.

Submitted (06-APR-1999) Hirofumi Uchimiya, University of Tokyo,
Inst. Mol. Callu. Biosci, Cellular Punction; 1-1-1 Yayoi,
Bunkuo-ku, Tokyo 113-0032, Japan
(E-mail:uchimiya@imcbns.iam.u-tokyo.ac.jp, Tel:81-3-3812-2910,
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                                                                                                                                                                    Fax:81-3-3812-2910)
On Mar 8, 2000 this sequence version replaced gi:6759252.
Sequence updated (02-Mar-2000)
Location/Qualifiers
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.9%; Score 351; DB 8; Length 1181; 66.4%; Pred. No. 9.7e-83; arive 0; Mismatches 255; Indels C
                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/product="Bax inhibitor-1"
/protein_id="BAA89540.3"
/db_xref="GI:7209772"
   FEBS Lett. 464 (3), 143-147 (1999)
                                                                                                                                                                                                                                                              /organism="Oryza sativa"
/strain="Yamahoushi"
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                     /gene="BI-1"
126. .875
/gene="BI-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 504; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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ORIGIN
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                       MEDLINE
REFERENCE
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| Jene="pB1-1" |
| Jene="bmx inhibitor 1" |
| Jene="bmx inhib
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Hordeum vulgare subsp. vulgare.
Hordeum vulgare subsp. vulgare
Eukaryota, Virighlantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Hordeum.
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Differential expression of putative cell death regulator genes
near-isogenic, resistant and susceptible barley lines during
interaction with the powdery mildew fungus
Plant Mol. Biol. 47 (6), 739-748 (2001)
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                                                                                                   726
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Huckelhoven,R.

Direct Submission
Submitted (22-JAN-2001) Huckelhoven R., Institute for Phytopatholyg and Applied Zoology, Justus-Liebig-University Giessen, Heinrich-Buff-Ring 26-32, 35392 Giessen, GERMANN Location/Qualifiers
646 cciscascricaretricascritacriticaccietrarcritcricascricascria
                                                                                                               TTGACACCCAAGAAATTATTGAGAAGGCTCACTTGGGTGATATGGATTACGTTAAGCATG
                                                                                                                                                                                                             706 ATGACACGCAGGAGATCATCGAGAGGGCTCACCACGGTGACATGGACTACATCAAGCACG
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Hordeum vulgare mRNA for BAX inhibitor ו (pBI-1 gene)
AJ290421
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(cultivax="Pallas")
(db xref="taxon:112509"
(tissue_type="leaf")
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llarity 67.4%; Pred. No. 3.1e-81;
Conservative 0; Mismatches 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     787 AGAATGCATCTGAGAAGAGAGAAGAAGAAGAAGAAGAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    826 AGAACGCGTCTGACAAGTCGGAGGAGAAGAAGAGGAAGA 864
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/dlone="RZ957"
/clone lib="eticlated leaf tissue of rice"
/clone lib="eticlated leaf tissue of rice"
/note="Westor: Lambda ZAP II/PBluescript, V-type: Plasmid;
A Lambda ZAP II/DNA library was constructed from mRNA
extracted from eticlated leaf tissue of the rice cultivar
'IR36' and converted to pBluescript (amp resistant) as
described in Causes et al. (1994) Genetics 138:1251-1274.
For insert amplification, Use MI3 forward and reverse
primers. Restriction site is ECORI. Clones from this
library are designated with the prefix 'RZ'."
<11..418 c 124 g 116 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is a partial sequence of the RFLP clone named above that was mapped at Cornell University Plant Breeding Dept. and sequenced at the Genome Sequencing Center at Cold Spring Harbor Laboratory. This marker is located on rice chromosome 2. For citations and other related information concerning this probe, please refer to the Gramene database at http://www.Gramene.org.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 TGCTGGGGCTTACCTTCACATTCTATGGAATATCGGTGGCCTCCTCACAACAATGGCTTG 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 cerededadaktos et derrerrerrencia et et a ceredadada et a 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              422 CATTAACTTCGATCCAAGCATTGTGTTTTGGCGCTTTTGTAGGTTGTGCTGTGGTTTTTGG 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.3%; Score 178.6; DB 11; Length 65.2%; Pred. No. 1.1e-36; trive 0; Mismatches 140; Indels
                                     Email: srm4@cornell.edu
Primer A: M13 universal Forward GTAAAACCACGGCCAGT
Primer B: M13 Universal Reverse AACAGCTATGACCATG
STS size: 418
Protocol:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Oryza sativa"
/cultivar="IR36"
/db_xref="taxon:4530"
/map="2"
                                                                                                                                                                                                                                                                                                                                                                                                Sunits
                                                                                                                                                                                                                                                           Template: 20-100ng
Primer: 5pmol each
DNTPs: 40nmol
                                                                                                                                                                                                                                                                                                                                                                                  Tag polymerase: 5u:
Total volume: 50ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tris-HCl: 100mM
KCl: 500mM
MgCl2: 15mM
Gelatin: 0.1%
PH: 8.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 65.2
Matches 262, Conservative
Fax: 6072556683
                                                                                                                                                                                                                                                                                                           Primer:
DNTPs: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ಠ
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Oryza sativa.

Bukaryota, Varidiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryzeae; Oryza.

1 (bases I to 418)
McCouch, S.R.
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                                                                                                                                                                                                                                                           223 GIGCITIAGIGGCAICGGCIGCIGGGGCITACCTICACATICIAIGGAATAICGGIGGCC 282
                                                                                                                                                                                                                                                                                                                              128 TIGCACTGGCCTCATCTGCCGGGGGGTGCTTACCTACACATTGCCCTGAACATCGGCGGGA 187
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67
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CCTTCTACTCGACCTCGTCGGCGGCGGCGAGCGGCTGGGGCCACGACTCCCTCAAGAACT
                                                                                     163 TCCGCCAGATCTCACCTCTCGTTCAACTCATCTCAAGCAGGTGTACCTTACGCTATGCT
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Cornell University
Dept. of Plant Breeding, Ithaca, NY 14853-1901, USA
Tel: 6072550420
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STS.
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Unpublished (2002)
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Gaps

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LOCUS DEFINITION

RESULT 12 G73645

668 823 728 ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

541 372

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Query Match 12.1%; Score 125.2; DB 9; Length 892; Best Local Similarity 52.2%; Pred. No. 1.9e-22; Matches 358; Conservative 0; Mismatches 313; Indels 15;
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/db_xref="taxon:9606"
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                                                                                                                                 808 AGAAGAAGAAGAAGAGAGAAA 829
                                                                                                                                                                 120 AAGACGAGAAGAAGAAGAA 99
                                                                                                                                                                                                                                                                                                                  AF033095.1 GI:2645728
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/gene="TEGT"
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Homo sapiens
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                                                                                                               G71526
360 bp DNA linear STS 08-JUN-2001
A61521534FMo17 maize leaf DNA Zea mays STS genomic, sequence tagged
                                                                                                                                                                                                               Zea mays.

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (Dases 1 to 360)

1 (Dases 1 to 360)

3 UTR sequences of maize genes
Uppublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 TCTACTITGGCCTCCTGGTTTTTCCTGGGATATATGGTGTTTGACACCCAGGAGATCATCG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       568 TCTGGTTGCACTTTGCATCCTCCATTTTTGGTGGTTCCATGGCTGTTTTCAAGTTTGAGT 627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       628 TGTATTTTGGACTCTTGGTGTTTTGTGGGCTACATCGTCTTTGACACCCCAAGAAATTATTG 687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="DE811"
|db_xref="taxon:4577"
|Cione lib="maize leaf DNA"
|note="PCR products amplified from genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Denaturation: 94 degrees C for 30 seconds Annealing: 60 degrees C for 45 seconds Polymerization: 72 degrees C for 90 seconds PCR cycles: 31
Thermal cycler: Perkin Elmer TC
542 TCTTTCATCAGCGTCTCCCTTCTTCTGGTTGCACTTTGC 583
373 GCTCTTTCTGGCCTCTCCATCCTGCTCTGGCTGCAGTTTGC 414
                                                                                                                                                                                                                                                                                                                                                                                                               Iowa State University
6405 Agronomy Hall, Ames, IA 50011, USA
741: 515-294-0975
Fax: 515-294-229
Enail: schnable@iastate.edu
Primer A: CAATTCATCAGCAGCTACC
Primer B: CGACTTGTTATTGACTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Template: 10-20 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Tag Polymerase: 0.05 units/ul
Total vol: 20 ul
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KC1: 50 mM
Tris-HC1: 20 mM
PH: 8.4.
Location/Qualifiers
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Schnable laboratory
                                                                                                                                                  G71526
G71526.1 GI:14333211
STS.
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a 87 c
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Matches 184; Conservative
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BASE COUNT
ORIGIN
                                                                               RESULT 13
G71526/c
LOCUS
DEFINITION
                                                                                                                                                             ACCESSION
VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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892 bp mRNA linear PRI 27-NOV-1997
Homo sapiens testis enhanced gene transcript protein (TEGT) mRNA,
AP033095
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RKLMMILAMNEKDKKKKKKK
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/gene="TEGT"
/note="small transcript; similar to human TEGT large
transcript encoded by GenBank Accession Number X75861 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
Cowling, R.T. and Birnboim, H.C.
Direct Submission
Submistered (15-NOV-1997) Cancer Research Group, Ottawa Regional Cancer Centre, 501 Smyth Road, Ottawa, ON KIH BL6, Canada
Location/Qualifiers
240 AGAGGGGCACCGTGGGGACATGGACTACATCAAGCACGCGCTGACTCTCTTCACCGACT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 tricatecectriraaaartricecararaaecececeaeaecaecaecaeaaaaa 149
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                                                                                                748 TIGGCGCTGTTTTTGTGCGGATTCTGATCATCATGTAAAGAATGCATCTGAGAAGAAG 807
                                                                                                                                                                           180 mentecentenenterancencinencinentaneaneaneaneacaeacaeaanee 121
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Pred. No. 1.8e-22;
0; Mismatches 313; Indels
                                                                                                                      /db_xrefe"taxon:9606"
/dlone="MGC:5230 IMAGB:2900280"
/tlssue_type="Hacenta, choriocarcinoma"
/tlone_lib="NIH MGC_10"
/lab_host="DH10B"
/note="Vector: pGWV-SPORI6"
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                                                             organism="Homo sapiens"
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Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Contact: villalon.b.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia, A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W., Muzny, D.M., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLML at: http://image.llml.ggv
Series: IRAK Plate: 3 Row: k Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 2645728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2609)
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Submitted (16-NOV-2000) National Institutes of Health, Mammalian
Submitted (16-CO) (2000) Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                     491
                                                                                                                                                                                                                              390 AACCCCAGCATCCTTCCCACTGCTTTCATGGCCACAGCAATGATCTTTACCTGCTTCACC 449
                                                                                                                                                                                                                                                                                                                                                                   450 CICAGIGCACTCIAIGCCAGGCGCCGIAGCIACCICITICIGGGAGGIAICTIGAIGICA 509
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                                                                                                 330 doarridearrecriacadoarroccriodecerioeceriodadiriridarirecrore 389
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                                   372 GCAGCIGCACTTTTTGAAGGCGCCTCTATTGGTCCTCTGATTGAGCTGGGCATTAACTTC
                                                                                                                                                                     432 GATCCAAGCATTGTGTTTTGGCGCTTTTTGTAGGTTGTTGTGGTGTTTTTTGGTTGCTTCTCA
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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COMMENT
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Db 750 GAAAAGGATAAGAAAAAAGAGAAGAA 775

Search completed: May 25, 2003, 11:00:16 Job time : 2754 secs

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May 25, 2003, 08:47:18 ; Search time 284 Seconds (without alignments) 8199.177 Million cell updates/sec
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ALIGNMENTS

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Arabidopsis thaliana, plant; insecticide, fungicide, transgenic, stress; disease, crop; thale cress; tolerance factor; insect; pathogen; nutrition; ds.
                                                                       Arabidopsis thaliana expressed polynucleotide SEQ ID NO 223.
                ABN98455 standard; DNA; 1009 BP
                                                                                                                                                                                    26-JAN-2001; 2001US-0770445.
                                                                                                                                                                                                      27-JAN-2000; 2000US-178472P.
                                                     01-AUG-2002 (first entry)
                                                                                                                                                                                                                        GORLACH J.
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HAMILTON C M.
PRICE J L.
RAINES T M.
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PRAMEAKA J G.
PAGE A.
                                                                                                                             Arabidopsis thaliana.
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(PAGE/)
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        ABN98455
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RESULT 1
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New Arabidopsis thaliana nucleic acid for identifying homologous genes, producing compositions that modulate the expression or function of its encoded protein, and mapping functional regions of protein
                                                                                Hamilton CM, Price JL, Raines TM, Yu Y,
A, Mathew AV, Ledford BL, Woessner JP, Haas
A, Slater T, Davis KR, Allen K, Hoffman N,
                                                                                                                                                           Claim 1; SEQ ID NO 223; 49pp + Sequence Listing; English
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Page A, Ma
Kricker M,
MATHEW A V.
LEDFORD B L.
WOESSNER J P.
HAAS W D.
                         GARCIA C A.
KRICKER M.
SLATER T.
DAVIS K R.
ALLEN K.
HOFFMAN N.
                                                                                                                 WPI; 2002-400781/43.
                                                                   HURBAN P.
                                                                                Gorlach J, Rameaka JG,
Garcia CA, 1
Hurban P;
                   (HAAS/)
(GARC/)
(KRIC/)
(SLAT/)
(DAVI/)
(ALLE/)
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The invention relates to an Arabidopsis thaliana nucleic acid (I)

Comprising a sequence Gapable of hybridising under stringent conditions
to a sequence selected from any one of 999 sequences (ABN99231-ABN99231),
given in the specification or lits fragment. A polypeptide (II) encoded by
given in the specification or lits fragment. A polypeptide (II) encoded by
Given in the specification or lits fragment. A polypeptide (II) encoded by
Given in the specification or lits fragment. A polypeptide (II) is
useful for screening a candidate agent for its biological effect. (I) is
useful in identifying monologues or related genes, in producing
compositions that modulate the expression or function of its encoded
compositions that modulate the expression or function of its encoded
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compositions that capacity is agents are useful in improved methods of treating
crops to prevent or treat disease. (II) are also useful in screening
crops to prevent or treat disease. (II) are also useful in a companient to the action of interest, for establishing the extent to which
crops to prevent or treat disease. (II) are also useful in a proteins of interest, for establishing the extent to which
any specific insect and/or pathogen is responsible for damage to a
crop structular plant, for identifying other mediators that may induce
configurable plant, for identifying other mediators that may induce
configurable plant, for identifying other mediators that may affect the biological function of the gene or gene products
configurable. (IV) is useful in the study of genetic den ecification, but was obtained in electronic format esegdata.uspto.gov/sequence.html?DocID=999909770445

Query Match

41.5%; Score 428.8; DB 24; Length 1009;
Best Local Similarity 73.7%; Pred. No. 4.1e-115;
Matches 560; Conservative 0; Mismatches 197; Indels 3; Sequence 1009 BP; 243 A; 201 C; 218 G; 347 T; 0 other;

72 AAGAAGAAGAAGAATGGAAGGTTTCACATCGTTCGTTCGACTCGCAATCTGCCTCTCGC 131 23 AAAAAAAGAAAGAAAGGATGCGTTCTTCTTCTTCGATTCTCAACCTG---GTAGC 79 3; Gaps

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132 AACCGCTGGAGTTATGATTCTCTCAAAACTTCCGCCAGATCTCAACCTCGTTCAAACT 191

99US-0121825. 99US-0123180. 99US-0123548. 99US-0125788.

25-FEB-1999; 05-MAR-1999; 09-MAR-1999; 23-MAR-1999;

559 619 731 679 259 319 499 671 ACCCTTTTCACAGATTTTGGCGCTGTTTTTGTGCGGATTCTGATCATCATGTTAAAGAAT 791 680 Accertiticacidacitificadeticificiticedatificatearadigiticadadae 739 311 371 431 379 491 439 551 611 80 AGAAGCTGGAGCTATGATTCTCTTAAAACTTCCGTCAGATTTCTCCAGCCGTTCAGAAT 139 TACCTTCACATTCTATGGAATATCGGTGGCCTCCTCACAACAATGGCTTGCATGGGAAGC <u>raccirccargracregaanarcggcggrarrcrracaacgargargrarrggaacr</u> ATGGTGTGGCTTCTCTCAGCTCCTTCTATCAAGAGCAAAAAGGGTGGCTCTTCTGATG GCAGCTGCACTTTTGAAGGCGCCTCTATTGGTCCTCTGATTGAGCTGGGCATTAACTTC 320 ecerciecrericipalagerecricitaticaccecricarcalagical 380 GACCCAAGCATCCTTATCACTGCGTTTGTTGGAACTGCGATAGCGTTTGTCTGTTTCTCA GCTGCTGCCATGTTGGCAAGGCGCAGGAGTACTTGTACCTCGGGGGCCTTCTTTCATCT 440 geaceacaargiraceaagacecaccacacrarciciacerrocaccaccacrarci 612 GITITICAAGIITIGAGIIGIAITITIGGACTICITIGGIGITITIGIGGGCTACATCGICITITIGAC seo arcritaagrirgagrigiacririgaacriritgarcrirgigggaracarggragiggac 620 acacaadadatraradaaaadgcacacccccgrdacardgacriagardraaaacarrcgrd carcitaaaceeerriarrieaccriarererecerrererererecercreecringeacer 260 Argarriegerecrirchererecrerrangaacaccaaaaaagerrrererererr GATCCAAGCATTGTGTTTGCGCGCTTTTGTAGGTTGTGCTGTGGTTTTTGGGTTGCTTCTCA GGCGTCTCCCTTCTCTGGTTGCACTTTGCATCCTCCATTTTTGGTGGTTCCATGGCT CATCTCAAGCAGGTGTACCTTACGCTATGCTGTGCTTTAGTGGCATCGGCTGCTGGGGCT Hybridisation assay, genetic mapping, gene expression control, protein identification, signal transduction pathway, metabolic pathway, promoter, termination sequence, ss. Arabidopsis thaliana DNA fragment SEQ ID NO: 21973 792 GCATCTGAGAAGGAAGAAGAAGAAGAAGAGAGAAACT 831 740 TCAGCAGATAAAGAAGAAGAAGAAGAAAAAGGAGAAACT 779 AAC38715 standard; DNA; 1066 25-FEB-2000; 2000EP-0301439. 17-OCT-2000 (first entry) Arabidopsis thaliana EP1033405-A2 06-SEP-2000 AAC38715; 200 552 732 672 252 432 140 372 492 192 312 RESULT 2 AAC38715 à ò d g ò ઠે 셤 g à ò g d à d ò d ö g à

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(FLET-) FLETCHER CHALLENGE FORESTS LTD.
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                                                                                                                                                                                                                                                                                                                                     AAF44782 standard; cDNA; 884
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P-PSDB; AAB65755.
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99US-0161404
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The present invention relates to coding sequences (see AAP44740-F44840 and AAF44843-F44844) and proteins (see AAB65714-B65814) involved in programmed cell death (PCD; apoptosis). The coding sequences and proteins of the present invention are useful for modulating a PCD or cell death pathway and various developmental pathways in a forestry plant, by eathy incorporating one of the present coding sequences into the genome of the forestry plant, where the coding sequence provides a PCD pathway that is not present in a native form of the forestry plant.
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                                                                         630 ACACAAGAGATTATAGAAAAGGCACACCTCGGTGACATGGACTATGTAAAACATTCGTTG
Query Match
21.4%; Score 221.2; DB 22; Length 884;
Best Local Similarity 60.6%; Pred. No. 2.6e-54;
Matches 383; Conservative 0; Mismatches 243; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell death modulator; programmed cell death; PCD; apoptosis;
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Novel defender against cell death polynucleotide useful for modulating programmed cell death pathway and specific development pathways in forestry plant .
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                                                                               The present invention relates to coding sequences (see AAF44740-F44840 and AAF44443-F44844) and proteins (see AAB65714-B65814) involved in programmed cell death (PCD; apoptosis). The coding sequences and proteins of the present invention are useful for modulating a PCD or cell death pathway and various developmental pathways in a forestry plant, by stably incorporating one of the present coding sequences into the genome of the forestry plant, where the coding sequence provides a PCD pathway that is not present in a native form of the forestry plant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
21.2%; Score 219.2; DB 22; Length 527;
Best Local Similarity 74.5%; Pred. No. 7.7e-54;
Matches 289; Conservative 0; Mismatches 98; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 527 BP; 98 A; 148 C; 143 G; 138 T; 0 other;
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                            Claim 1; Pages 62-63; 142pp; English
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99US-0123548.
99US-0125788.
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
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905-012626 905-012676 905-0127676 905-012873 905-012873 905-013043 905-013043 905-013144 905-013246 905-013246	99UG-0133487 99UG-0132863 99UG-0132865 99UG-0134218 99UG-0134219 99UG-0134370 99UG-0134370 99UG-0134370 99UG-0134370 99UG-0134370 99UG-0134370 99UG-0134370 99UG-0137522 99UG-0137728 99UG-0137728 99UG-0137728	905-013911 905-013945 905-013945 905-013945 905-013945 905-013945 905-013945 905-013945 905-013945 905-013945 905-013945	905-014035 908-014035 908-014035 908-014089 908-014089 908-014205 908-014205 908-014205 908-014209 908-014509 908-014509 908-014509 908-014509
5. MAR. 1999; 1. MAR. 1999; 6. APR. 1999; 9. APR. 1999; 1. APR. 1999; 1. APR. 1999; 3. APR. 1999; 6. APR. 1999; 6. MAY. 1999; 6. MAY. 1999; 6. MAY. 1999; 6. MAY. 1999; 6. MAY. 1999; 6. MAY. 1999;	06-WAY-1999; 11-WAY-1999; 14-WAY-1999; 14-WAY-1999; 14-WAY-1999; 11-WAY-1999; 11-WAY-1999; 22-WAY-1999; 22-WAY-1999; 22-WAY-1999; 25-WAY-1999; 03-UN-1999; 03-UN-1999; 04-UN-1999; 04-UN-1999; 04-UN-1999; 06-UN-1999;	#-CUN-1999; -CUN-1999; -CUN-1999; -CUN-1999; -CUN-1999; -CUN-1999; -CUN-1999; -CUN-1999; -CUN-1999; -CUN-1999; -CUN-1999; -CUN-1999; -CUN-1999; -CUN-1999; -CUN-1999; -CUN-1999; -CUN-1999;	1. CUL 1999; 1. CUL 1999;
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GENESIS RES & DEV CORP LID.
NEW ZEALAND PASTORAL AGRIC RES INST LTD.
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            Bovine; mammary
                                                     WO200114553-A1
                                                                                                                   23-AUG-1999;
                                  Bos taurus,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGGTGTGGCTTCTCTCAGCTCCTTATCAAGAGCAAAAAGGGTGGCTCTTCTGATG 371
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99US-0158232.
99US-0158369.
99US-0159293.
99US-0159295.
99US-0159330.
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99US-0159634.
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Matches 278; Conserv
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New polypeptides and polynucleotides encoding the polypeptides, which mammery gland tissue, useful for stimulating mammery gland growth or function, or inducing differentiation of milk producing cells -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -- CATTCTATGGAATATCGGTGGCCTCCTCACAACAATGGCTTGCATGGGAAGCATGGTG 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.5%; Score 128.8; DB 22; Length 873; Ilarity 52.5%; Pred. No. 3.1e-27; Conservative 0; Mismatches 328; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to proteins derived from bovine mammary gland cells. The invention is useful for stimulating bovine mammary gland cell growth and function, inhibiting the growth of vaculus mammary gland cancer cells, inhibiting the angiogenee's and vascularization of tumours, or modulating the growth of blood vessels in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 873 BP; 206 A; 218 C; 196 G; 253 T; 0 other;
Grigor MR, Molenaar AJ;
                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 43; 97pp; English.
                                                                           WPI; 2001-226619/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 386; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            612
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gland; cancer; tumour; angiogenesis;

99US-0150330

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cardioactive; immunomodulatory; muscular active; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynecological; antibacterial; diagnosis; neural disorder; immune disorder; reproductive; proliferative disorder; wound healing; infectious disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer associated proteins represented in AA558106 - AA558846. Lung cancer associated proteins and polynucleotide sequences, their agonists, and antagonists may have neuroprotective; cytostatic; cardioactive; limmunomodilatory; muscular active general; vulnerary; gastrointestinal general; nephrotropic; antiinfective; gynecological; or antibacterial activity. The invention also includes antibodies specific for the protein or polynucleotide sequences. The hum and ander associated polynucleotide sequences. The protein may be used for detection of lung cancer, chromosome identification, as chromosome markers, and for numerous etheromographic research purposes. The proteins may be used to treat, adjagnostic or research purposes. The proteins may be used to treat, disorders such as neural; immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer associated gene sequences, referred to as lung cancer
gens, useful for treatment, prevention, and diagnosis of disorders
                                                                                                                                                                         714
                    594
                                                        731
                                                                                            654
                                                                                                                                   791
                                                                                                                                                                                                                 GCATCTGAGAAGGAAGAAGAAGAAGAAGAAGAGAGAAACTAGATTTGCTTCTCAACTTGT 851
                                                                                                                                                                                                                                                     715 G-----agaadgaraagaagaagaagrgaagcagccarccagccrrgcccarrrg 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, lung cancer associated protein, neuroprotective, cytostatic,
535 CITITCCAGGCAAACCIGIATATAGGGGCIGGIGGTCAIGIGGCTITGICCTITITGAT
                                                        655 GACCICTICITGGATTICGTAACTCTTTCAGAAAGCTCATGATGATCCTGGCTATGAAT
                                                                                                                                   732 ACCCITTICACAGAITITIGGCGCIGITITIGIGCGGAITICIGAICAIGITAAAGAAI
                                                                                            595 ACTCAACTCATTATTGAAAAGGCTGAAAATGGAGATAAAGATTATATCTGGCACTGCGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lung cancer associated polynucleotide sequence SEQ ID 73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 550-551; 1425pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                  ద
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF18054 standard; DNA; 2922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAR-2000; 2000WO-US05918.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                          852 GGTTTCCANAACTCC 866
                                                                                                                                                                                                                                                                                                                                  769 ACTICCICICCCICC 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antigens, useful for
such as lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-587514/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENC
(ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAB58178
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disorders. The proteins may also be used in the treatment of wounds and infectious diseases. Polymucleotide sequences AFF18425 - AFF18433 and peptide AABS8549 are used in the course of the invention for the identification and characterisation of the polymucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             440
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                                                                                                                                                                                                                                                                                                                                                                            Score 125.2; DB 21; Length 2922;
Pred. No. 6.5e-26;
0; Mismatches 313; Indels 15;
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viral infection; parasitic infection, protozoal infection;
                                                                                                                                                                                                                                                                                 Sequence 2922 BP; 712 A; 686 C; 654 G; 863 T; 7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GADADGGATAAGAAGAAGAAGAA 823
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                                                                                                                                                                                                                                                                                                                                                                  12.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 52.2
Matches 358; Conservative
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                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Homo sapiens.
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rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; crohn's disease; ulceraive colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
fungal infection; sterile inflammatory disease; psoriasis;
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WO200228999-A2

11-APR-2002

03-OCT-2001; 2001WO-US30821.

03-OCT-2000; 2000US-237189P

(GENE-) GENE LOGIC INC

Vockley J; Yamaga S, Beazer-Barclay Y, Weissman SM,

VPI; 2002-435328/46

expression Detecting granulocyte activation by detecting differential expression genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity

Claim 1; SEQ ID No 1229; 114pp; English.

The invention relates to detecting (MI) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (GS) identified by the chief analysis as given in the specification, and comparing the expression level in an unactivated of GCA, where differential expression level in an unactivated GC, where differential expression of GS is indicative of GCA and that alters the expression of GS is indicative of GCA with an agent capable of modulating (M2) GA by contacting GC with an agent capable of modulating (M2) GA by contacting GC with an agent capable of modulating (M3) is a mallergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene (s) from GS, where the level of expression of the gene is indicative of inflammator).

(4) It reating (MS) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammatory disease, by contacting a tissue having of the detecting an inflammation with a magnet that modulates the expression or sterile for ground in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting an inflammation in a tissue, an allergic cresponse in a subject, exposure of a subject to a pathogen or sterile conflammatory disease (e.g. psoriate inflammatory disease (e.g. psoriate) in a tissue, an allergic cresponse in a subject, exposure of a subject to a pathogen or sterile response in a subject, exposure of a subject to a pathogen or sterile conflammatory disease (e.g. psoriate inflammatory disease (e.g. psoriate inflammatory bowel disease, crohn's disease, ulcerative colitis, persistic infection, protozoal infection, viral infection, protozoal infection, viral infection injury, when sec of the printed specification, but was obtained in electronic format directly from WIPO at form part ftp.wipo.int/pub/published_pct_sequences The sequence data for this patent

Sequence 2600 BP; 619 A; 621 C; 590 G; 770 T; 0 other;

Score 122; DB 24; Length 2600; Pred. No. 5.3e-25; 0; Mismatches 315; Indels 15; Query Match
Best Local Similarity 51.9%;
Matches 356; Conservative

317 259 247 371 307 427 487 611 544 671 731 664 791 724 127 GICTATGCAAGITTTGCCCTTTGTATGTTGTGCGGCGCCTGCAGGGGGCCTATGTCCATATG 187 431 367 491 551 545 CCTTTCCAGGCAAACCTGTATGTGGGACTGGTGGTCATGTGTGGCTTCGTCCTTGTTGAT 604 TATGATTCTCTCAAAAACTTCCGCCAGATCTCACCTCTCGTTCAAACTCATCTCAAGCAG 203 665 GATCTCTTAGATTTCATTACTGTCTTCAGAAAACTCATGATGATCCTGGCCATGAAT <u>trigatigoccitritaaaartricicatararaccoccicaaccacacacaccicaaaas</u> --CATTCTATGGAATATCGGTGGCCTCCTCACAACAATGGCTTGCATGGGAAGCATGGTG 188 GICACICALITCALICAGGCIGGCCIGCIGICAGCCITGGGCICCCIGALALIGAIGAIT TGGCTTCTCTCAGCTCCTCCTTATCAAGAG-----CAAAAAAGGGTGGCTCTTCTGATG rescriearescaacacercarascearesaacreaacacaaaaacrescarereer GGATTIGCATICCITACAGGAGITGGCCTGGGCCTGCCCTGGAGTTTTGTATTGCTGTC 368 AACCCCAGCATCCTTCCCACTGCTTTCATGGCCACAGCAATGATCTTTACCTGCTTCACC 492 GCTGCTGCCATGTTGGCAAGGCGCAGGGAGTACTTGTACCTCGGGGGCCTTCTTTCATCT CICAGIGCACICTAIGCCAGGCGCCGIAGCIACCICTIICIGGAGGIAICTIGAIGLA GEGGICTCCCTTCTCTGGTTGCACTTTGCATCCTCCATTTTTGGTGGTTCCATGGCT GCCCTGAGCTTGTTTGTCTTCCCTGGGGAAT---GTTTTCTTTGGATCCATTTGG GTTTTCAAGTTTGAATTGTATTTTGGACTCTTTGGTGTTTTGTGGGCTACATCGTCTTTGAC 732 ACCCTTTTCACAGATTTTGGCGCTGTTTTTGTGCGGATTCTGATCATCATGTTAAAGAAT GATCCAAGCATTGTGTTTTGGCGCTTTTTGTAGGTTGTGCTGTGGTTTTTTGGTTTGCTTCTCA GCAGCTGCACTTTTGAAGGCGCCTCTATTGGTCCTCTGATTGAGCTGGGCATTAACTTC GIGIACCITACGCIAIGCIGIGCITIAGIGGCAICGGCIGCIGGGGCIIACCIICA-Bax inhibitor; BI-1; human; apoptosis; ss GCATCTGAGAAGGAAGAAGAA 817 Location/Qualifiers 725 GAAAAGGATAAGAAGAAGAGAGAA 750 AAV59067 standard; cDNA; 2634 98WO-US05015. 02-FEB-1999 (first entry) Bax inhibitor BI-1 cDNA. Homo sapiens WO9840397-A1 13-MAR-1998; 17-SEP-1998 AAV59067; 144 128 318 372 308 428 552 488 672 792 89 204 260 248 432 612 RESULT 9 AAV5906° g 셤 g 엄 g ò δ 셤 g à g 8 ò ઠે g à ò d ઠે 엄 $\dot{\delta}$ ò 음 à

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                                                                                                                                                                                                                                                                                                                                                                       This cDNA clone codes for an inhibitor protein, termed BI-1 (see AAW33186), of the pro-apoptotic protein Bax. Nucleic acids encoding BI-1 and BI-2 (see AAW59068) were identified by suppression of Bax-induced death of yeast cells transformed to express human Bax. A human H902 cDNA library was used for library screening. The invention provides vectors, optionally expression or viral vectors, ontaining BI modelic acids, and host cells containing these vectors. The nucleic acids, and host cells containing these nortains of these proteins in cells, or antisense molecules prepared from them used to decrease expression. In these ways, cellular apoptotic activity may be modulated (claimed). The nucleic acids and complementary sequences are also useful as probes to detect BI-encoding nucleic acid molecules in samples.
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Best Local Similarity 51.9%; Pred. No. 5.4e-25;
Matches 356; Conservative 0; Mismatches 315; Indels 15; Gaps
                                                                                                                                                                                                                              Bax inhibitor proteins, BI-1 and BI-2 - useful e.g. to modulate cellular apoptotic activity or identify agents altering BI-1 or BI-2 binding which can modulate apoptotic activity
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                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 61-63; 80pp; English.
                  97US-0818514.
                                                               (BURN-) BURNHAM INST
                                                                                                                                                            WPI; 1998-531519/45
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                                                                                                            Reed JC, Xu Q;
               14-MAR-1997;
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The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to CDNAs encoding them (ABP54131-ABD56305), and also encompasses polypeptides 90% identical and polymuchorides 90% identical and polymuchorides dentical to the sequences of the invention. The invention additionally relates to to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polymucleotides and polypeptides in diagnosing, of ovarian antigen polymucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast cancer, and disorders (e.g., infertility, disorders of pregnancy, anovulation, or polycystic ovariant orders of pregnancy, anovulation, polycystic ovariants of include ovarian cancer and breast cancer, and disorders, infertility, disorders of pregnancy, anovulation, ordinored, inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficancies, autocimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; pCOS; ovarian cyst; dysmenorthoes; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; gene; ss.
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ACCCTTTTCACAGATTTTGGCGCTGTTTTTGTGCGGATTCTGATCATCATGTTAAAGAAT 791
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                                                                                          GATCTCTTTAGATTTCATTACTGTCTTCAGAAACTCATGATGATCCTGGCCATGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human ovarian antigen HPDWT56 cDNA, SEQ ID NO:1953.
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                                                                                                                                                                                                GCATCTGAGAAGGAAGAAGAA 817
                                                                                                                                                                                                                                                                                          GAAAAGGATAAGAAGAAAGAGAA 782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABQ56073 standard; cDNA; 751
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respiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and bolynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, durg targeting and phenotyping. The present sequence represents cDNA encoding a human ovarian antigen of the
                                                                                                                                                                                                                  Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                           8.1%; Score 83.8; DB 24; Length 751; 50.6%; Pred. No. 4.3e-14; vative 0; Mismatches 288; Indels 16;
                                                                                                                                                                                                                                                                                                      Sequence 751 BP; 163 A; 177 C; 185 G; 225 T; 1 other;
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Matches 312; Conservative
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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. S' EST are derived from mRNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                    Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
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Pred. No. 3e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Giordano J;
Human secreted protein 5' EST, SEQ ID NO: 8293
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Similarity 53.7%;
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188 TGATGATCCTGGCCATGAATGAAAGGATAAGAAGAAGAAGAAGAAGAA 143

AAV86028 standard; cDNA; 520 BP

RESULT 13

g

(first entry)

27-APR-1999 AAV86028;

EST clone B115.

human;

Expressed sequence tag; secreted protein; haematopoiesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; hu chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.

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expressed in cancer tissues. ABB/9933 to ABB/9004 represent proteins encoded by the ABG/076 to ABG/0787 nucleic acid sequences. (I) can be used in antisense therapy, An antibody immunoreactive with a polypebtide used in antisense therapy. An antibody immunoreactive with a polypebtide or detecting the presence or absence of a polymucleotide encoded by a nucleic acid which hybridises to (I) in a cell. A probefyziner derived trom (I) can be used for determining the presence of a nucleic acid which hybridises to (I), and for determining the presence of a nucleic acid which phypridises to (I), and for determining the presence of cells from a patient. (I) is useful for determining the presence of colon cancer in a cell or tissue type, for determining the presence of state of other type of cancer, in antisense therapy, to generate macroarrays on a solid surface, to identify a chromosome on which the corresponding gene resides, and in tissue profiling, forensics, genetic analysis, mapping and diagnostic applications. (I) can be used to raise the action of the corresponding and diagnostic applications. (I) can antibodists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid that is differentially expressed in cancer tissues useful for determining the presence of colon cancer in a cell or tissue type, and in antisense therapy .
                                                                                                                                                                                               Human; colon cancer; cancer; tissue profiling; forensic; mapping;
genetic analysis; diagnostic; antisense therapy; gene; ss.
                                                                                                                                                       Human colon cancer related nucleotide sequence SEQ ID NO:2922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.2%; Score 74; DB 24; Length 595; 58.0%; Pred, No. 2.9e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dwivedi P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 595 BP; 180 A; 124 C; 130 G; 155 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Catino TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carroll E,
                                       ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 1; 796pp; English.
                        9227/c
ABQ59227 standard; cDNA; 595
                                                                                                                                                                                                                                                                                                                                                                                     02-OCT-2001; 2001WO-US30732.
                                                                                                                                                                                                                                                                                                                                                                                                                               02-OCT-2000; 2000US-237271P
                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Burgess C, Astle JH, Ca
Thiaglingam A, Lewis ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-426115/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (FARE ) BAYER CORP.
                                                                                                                                                                                                                                                                                                      WO200229086-A2
                                                                                                                    02-AUG-2002
                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                            ABQ59227;
RESULT 12
ABQ59227/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents an expressed sequence tag (EST), and is a polynucleotide of the invention. The polynucleotides of the invention are all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cabherin/tumour invasion suppressor activity, tumour inhibition activity. The EST sequences are also stated to be useful for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -- CATICTATGGAATATCGGTGGCCTCCACAACAATGGCTTGCATGGAAGCATGGTG 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 TATGATTCTCTCAAAAACTTCCGCCAGATCTCACCTCTCGAAACTCATCTCAAGCAG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204 GIGIACCTIACGCIAIGCIGIGCTIIAGIGGCAICGGCIGCIGGGGGCTIACCTICA---- 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 drerangenaringederingraherindegedegedengedegedenare 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
7.0%; Score 72; DB 20; Length 520;
Best Local Similarity 51.1%; Pred. No. 1e-10;
Matches 227; Conservative 0; Mismatches 205; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 520 BP; 103 A; 140 C; 123 G; 154 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 94; 633pp; English.
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Gaps

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95; Indels

0; Mismatches

Best Local Similarity 58.0 Matches 131; Conservative

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652 TGGGCTACATCGTCTTTGACACCCAAGAAATTATTGAGAAGGCTCACTTGGGTGATATGG

592 TITITGGTGGTTCCATGGCTGTTTTCAAGTTTGAGTTGTATTTTGGACTCTTGGTGTTTG 651

308 graditicitititaniatria aktranta akt

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248 ATTATATCTGGCACTGCATTGATCTCTTAGATTTCATTACTGTCTTCAGAAAACTCA 189

772 TGATCATCATGTTAAAGAATGCATCTGAGAAGGAAGAAGAAGAA 817

712 ATTACGITAAGCAIGCAIIGACCCIITIICACAGAITIIIGGCGCIGITIIIGIGGGAIIC 771

711

New polynucleotides encoding human secreted proteins - derived e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pitultary, retina and colon cDNA libraries

Merberg D;

McCoy JM,

Lavallie ER, Treacy M;

Agostino MJ, Jacobs K, Racie LA, Spaulding V, WPI; 1999-070076/06.

(GEMY) GENETICS INST INC.

98WO-US06954. 97US-0835913.

10-APR-1998; 10-APR-1997;

Molino GA;

15-OCT-1998.

WO9845435-A2

Homo sapiens

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                                                                                                292
                                                                                                                                                                                                                                                                                                                                                                                                                                  551
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                                                                                                                                                             431
                                                                                                                                                                                                                                                                                                 432 GATCCAAGCATTGTGTTTTGGCGCTTTTGTAGGTTGTGCTGGTTTTTGGTTGCTTGTTCA 491
                                                                                                                                                                                                                                                                                                                                                                  353 akoccekickirociroccacreciriroariesecaceseariearoriracorecireciroace 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   413 creadrichandechadedececesechactrititieseadenarenda 472
                                TGGCTTCTCTCAGCTCCTCTTATCAAGAG -----CAAAAAAGGGTGGCTCTTCTGATG 371
                                                                                                233 recercarecedacecretraracecareaacecaseaceaacaaaaaacececerecerecerecer
                                                                                                                                                                                                                             GGATTIGCATTCCTTACAGGAGTIGGCCTGGGCCCTGCAGCTTTTGTATTGCTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTGCTGCCATGTTGGCAAGGCGCAGGAGTACTTGTACCTCGGGGGCCCTTCTTCATCT
                                                                                                                                                                 GCAGCTGCACTTTTTGAAGGCGCCTCTATTGGTCCTCTGATTGAGCTGGGCATTAACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, colon cancer, cancer, tissue profiling, forensic, mapping, genetic analysis, diagnostic, antisense therapy, gene; ss.
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Thiaglingam A, Lewis ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCGTCTCCTTCTCTGGTTG 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           473 GCCCTGAGCTTGTTGCTTTTGTCG 496
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ABQ60318/c
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ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially expressed in cancer tissues. ABB78993 to ABB7904 represent proteins encoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be used in antisense therapy. An antibody immunoreactive with a polypeptide encoded by (I) is useful for detecting cancer in a patient sample, and for detecting the presence or absence of a polymodeotide encoded by a nucleic acid which hybridises to (I) in a cell. A probe/primar derived from (I) can be used for determining the presence of a nucleic acid which hybridises to (I), and for determining the phenotype of cells in a sample of cells from a patient. (I) is useful for determining the presence of colon cancer in a call or tissue type, for determining the presence of state of other type of cancer, in antisense therapy, to generate
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                                                                                                                                                                                                                                                                                           231
                                                                                                                                                                                                                                                                                                                                                                          230 ATTATATCTGGCACTGCATTGATCTTTCTTACATTTACTGTCTTCAGAAAACTCA 171
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                                                                                                                                                                 TITITIGGIGGILCCALGGCIGITICAAGITIGAGITGIATITIGGACICTIGGIGITIG 651
                                                                                                                                                                                                                                                  TGGGCTACATCGTCTTTGACACCCCAAGAATTATTGAGAAGGCTCACTTGGGTGATATGG 711
                                                                                                                                                                                                        349 irircrridgarccarrregecririrccadecaaaccrerargededecrecres 291
                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                      712 ATTACGTTAAGCATGCATTGACCCTTTTCACAGATTTTGGCGCTGTTTTTGTGCGGATTC
antibodies, and to screen for peptide analogues and antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human colon cancer related nucleotide sequence SEQ ID NO:1718.
                                                                            6.6%; Score 68.4; DB 24; Length 689;
llarity 59.3%; Pred. No. 1.3e-09;
Conservative 0; Mismatches 91; Indels 1.
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genetic analysis, diagnostic, antisense therapy, gene; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 rgargarccrggccargargaraaaggaraagaagaagagagaa 125
                                      Sequence 689 BP; 204 A; 157 C; 154 G; 158 T; 16 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carroll E, ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP
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ID ABQ58023 standard; cDNA; 506
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Thiaglingam A, Lewis
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                                                                                                  Best Local Similarity
Matches 134; Conserv
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                                                                                     Query Match
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macroarrays on a solid surface, to identify a chromosome on which the corresponding gene resides, and in tissue profilling, forensies, genetic analysis, mapping and diagnostic applications. (1) can be used to raise antibodies, and to screen for peptide analogues and antagonists.
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Sequence 506 BP; 150 A; 100 C; 105 G; 138 T; 13 other;

ä Gaps ۲, Query Match 5.9%; Score 61; DB 24; Length 506; Best Local Similarity 58.3%; Pred. No. 1.7e-07; Matches 120; Conservative 0; Mismatches 85; Indels

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283 ACTCAACTCATTATTGAAAAGGCCGAACATGGAGATCAAGATTATATCTGGCNCTGCATT 224

Search completed: May 25, 2003, 10:14:15 Job time : 290 secs

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Sequence 43, Appl
Sequence 44, Appl
                                                                                                                                                           May 25, 2003, 10:14:23 ; Search time 75 Seconds (without alignments) 4228.050 Million cell updates/sec
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Sequence 1, App
Sequence 1, App
Sequence 915, A
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Sequence 1, A
Sequence 1, A
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Sequence 3,
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1. /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2. /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3. /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

3. /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

3. /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*

3. /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*

5. /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-818-514-1
US-08-818-514-1
US-08-818-514-2
US-09-115-934A-1
US-09-115-934A-1
US-09-115-934A-1
US-08-93-36-2
US-08-93-36-2
US-08-93-36-2
US-08-93-440-14
US-08-93-140-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  441362 segs, 153338381 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                      OM nucleic - nucleic'search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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1034
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Perfect score:
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Sequence 17, Appl Sequence 7, Appli Sequence 17, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 368, Appl Sequence 28, Appl Sequence 20, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 5, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli	programmed cell the modification of forestry plant develd	Length 884;
3 US-09-128-155-17 4 US-09-111 470-7 1 US-08-328-554-5 1 US-08-465-293A-1 2 US-08-463-397A-1 3 US-09-102-977-1 4 US-09-103-977-1 4 US-09-643-597-368 4 US-09-453-702B-50 4 US-09-453-7702B-50 4 US-09-453-7702B-50 5 US-08-947-823-1 3 US-08-947-823-1 3 US-08-947-823-1 3 US-08-947-823-1 3 US-08-947-823-1 4 US-09-268-992-7 4 US-09-268-992-7	ing in 2A 2A	tch al Similarity 60.6%; Pred. No. 1.4e-52; 383; Conservative 60.6%; Pred. No. 1.4e-52; 383; Conservation 60.6%; Pred. No. 1.4e-52; 383; Conservative 60.6%; Pred. No. 1.e. 1.e. 1.e. 1.e. 1.e. 1.e. 1
31.6 31.6 31.6 31.6 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.3	RESULT 1 US-09-325-932A-43 US-09-325-932A-43 Sequence 43, Application US/09325932A Patent No. 6451604 GENERAL INFORMATION: APPLICANT: Flinn, Barry APPLICANT: Lasham, Annette TITLE OF INVENTION: Gompositions affect TITLE OF INVENTION: death and their use TITLE OF INVENTION: death and their use TITLE OF INVENTION: death and their use CURRENT APPLICATION NUMBER: US/09/325,93 CURRENT FILING DATE: 1999-06-04 NUMBER OF SEQ ID NOS: 206 SOFTWARE: FRASEQ for Windows Version 3 SEQ ID NO 43 LENGTH: 884 TYPE: DNA ORGANISM: Pinus radiata US-09-325-932A-43	et D
0 0, 000 0 000 000000000000000000000000	RESULT 1 US-09-322 FORCE	Ouery Matches 3 Oy 203 GG Oy 263 TC Oy 263 TC Oy 323 TC Oy 377 TG

556

304 AGCAÁTCACAGCAGGAGGAGGAATÁCCTATTTTGGGAGGATTATTGGGCTCGGGAAT 363 CICCCIICTCITCIGGIIGCACTITGCICCCCATTITIGGIGGIICCAIGGCIGIII 616

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497 TGCCATGTTGGCAAGGCGCAGGAGTACTTGTACCTCGGGGGCCTTCTTTCATCTGGCGT

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Pred. No. 1.4e-24;
0; Mismatches 315; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,514
FILING DATE:
CLASSIFICATION: 435
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4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                        APPLICANT: Reed, John C.
APPLICANT: Xu, Qunli
TITLE OF INVENTION: BAX Inhibitor Proteins
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores
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NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LT
TELECOMMUNICATION INFORMATION:
                                 Sequence 1, Application US/08818514
Patent No. 5837838
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: TENGTH: 2634 harryppen
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IBM PC compatible
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 356; Conserv
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CITY: San Diego
STATE: Californi
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TOPOLOGY: lin
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APPLICANT: Flin. Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of forestry plant develo
FILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
SUMBER OF SEQ IO NOS: 206
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 4.2e-52;
0; Mismatches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               797 TGAGAAGGAAGAAGAAGAAGAAGAGAGAA 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    604 CAGTAAATCCAGGGAAGGGAAAAAAAAGAGAA 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGCTGCTGCCATGTTGGCAAGGCGCAG 517
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Patent No. 6451604
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ilarity 74.5%;
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; ORGANISM: Pinus radiata
US-09-325-932A-44
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Matches 289; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
US-09-325-932A-44
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2415 GTCACTCATTTCATTCAGGCTGGCCTGCTGTCTGCCTTGGGCTCCCTGATATTGATGATT 2356
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,934A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09115934A
Patent No. 6130317
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Xu, Qunli
TITLE OF INVENTION: BAX Inhibitor Proteins
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
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CLASSIFICATION: 435
PRIOR APPLICATION: DATA:
APPLICATION NUMBER: US 08/818,514
FILING DATE: 14-MAR-1997
ATTORNEY/AGENT INPORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER: P-I
TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Diego
STATE: California
COUNTRY: United States
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ZIP: 92122
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US-09-115-934A-1
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                                                         318
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     520 GCCCTGAGCTTGTTTGCTTTTGTCCCTGGGGAAT---GTTTTCTTTGGATCCATTTGG 576
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                                                                                                    577 CTTTTCCAGGCAAACCTGTATGTGGGAACTGGTGGTCATGTGTGGCTTCGTCCTTTTTTGAT 636
                                                                                                                                                        637 ACTCAACTCATTATTGAAAAGGCCGAACATGGAGATCAAGATTATATCTGGCACTGCATT 696
                                                                                                                                                                                                                                                       732 ACCCTTTTCACAGATTTTGGCGCTGTTTTTGTGCGGATTCTGATCATCATGTTAAAGAAT 791
                                                                                                                                                                                                                                                                                                        697 GATCTCTTAGATTTCATTACTGTCTTCAGAAACTCATGATGATCCTGGCCATGAAT 756
                                                         612 GTTTTCAAGTTTGAGTTGTATTTTGGACTCTTGGTGTTTTTGTGGGCTACATCGTCTTTGAC
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Patent No. 5837838
GENERAL INFORMATION:
APPLICANT: Xu, Quni,
TITLE OF INVENTION: BAX Inhibitor Proteins
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BATCHIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,514
FILING DATE:
CLASSIFICATION: 435
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0; Mismatches 315;
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NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9
TELECOMMUNICATION INFORMATION:
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TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2634 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 4370 La Jolla Vi
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
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STRANDEDNESS: single
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US-08-818-514-2
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                                                                                                       2355 TGGCTGATGGCAACACCTCATAGCCATGAACTGAACAGAAAAAACTGGGACTTCTTGCT 2296
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TGGCTTCTCTCAGCTCCTCCTTATCAAGAG-----CAAAAAGGGTGGCTCT
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TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2634 base pairs
Tue May
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TYPE: nucleic acid STRANDEDNESS: single linear

TOPOLOGY: US-09-115-934A-1

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                                                                                                                144 TATGATICTCTCAAAAACTICCGCCAGATCTCACCTCTCGTTCAAACTCATCTCAAGCAG 203
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                                                             15;
      Length 2634;
Query Match
11.8%; Score 122; DB 3; Length 26:
Best Local Similarity 51.9%; Pred. No. 1.4e-24;
Matches 356; Conservative 0; Mismatches 315; Indels
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GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Xu, Qunli
TITLE OF INVENTION: BAX Inhibitor Proteins
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
                     Sequence 2, Application US/09115934A Patent No. 6130317
US-09-115-934A-2/c
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612 GITITCAAGITIGAGITGTAITITGGACTCTTGGTGTTTGTGGGCTACATCGTCTTTGAC

672

2115

2535 iridairedecirrrraaaarirrrerdarahaadedederaaredageagdacidaagaad 2476 2475 Grcharccaagrifigccccifighafgiffigigecdagagacchargrecarata 2416 2415 greacricarirearicadecridecrideriererecerridescreecridararerearidarir 2356 2295 dearmidcamiccimacadaaarmeeccheddccheccchedadrirmdramidcmerc 2236 2235 aaccecadeareerreecacracritraradoseacadearidareirraecridritade 2176 611 204 GIGIACCITACGCIAIGCIGIGCTITAGIGGCAICGGCIGCIGGGGGCTIACCITCA---- 259 GCTGCTGCCATGTTGGCAAGGCGCAGGGAGTACTTGTACCTCGGGGGCCTTCTTTCATCT 551 144 TATGATTCTCTCAAAACTTCCGCCAGATCTCACCTCTCGATCAAACTCATCTCAAGCAG 203 260 -- CATTCTATGGAATATCGGTGGCCTCCTCACAACAATGGCTTGCATGGGAAGCATGGTG TGGCTTCTCTCAGCTCCTCCTTATCAAGAG-----CAAAAAAGGGTGGCTCTTCTGATG 2355 regerigariegekaz ekerentago ekareka karanda karanda karanda ekerentago karanda ekerentago karanda 432 GATCCAAGCATTGTGTTTTGGCGCTTTTGTAGGTTGTGCTGTGGTTTTTGGGTTGCTTCTCA 2175 crcagrideacrerardeeaddeedaagaracracrerardagdagdrareraargargrea GGCGTCTCCCTTCTCTGGTTGCACTTTGCATCCTCCATTTTTGGTGGTTCCATGGCT 372 GCAGCTGCACTTTTTGAAGGCGCCTCTATTGGTCCTCTGATTGAGCTGGGCATTAACTTC Length 2634; Query Match
11.8%; Score 122; DB 3; Length 26
Best Local Similarity 51.9%; Pred. No. 1.4e-24;
Matches 356; Conservative 0; Mismatches 315; Indels STREET: San Diego
STATE: California
COUNTRY: United States
ZIP: 32122
CONDUTER READABLE FORM:
MEDIUM TYBE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATION
APPLICATION NUMBER: US/09/115,934
ATPORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 3209
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 2.
SEQUENCE CHARROTERISTICS:
LENGTH: LENGTH ACID ACID 700 4370 La Jolla Village Drive, Suite TYPE: nucleic acid STRANDEDNESS: single ; US-09-115-934A-2 Query Match 318 492 552 g g 엄 qq ò a δ à 셤 ò 원 ò ò

417 CIGGGCATTAACTTCGATCCAAGCATTGTGTTTTGCCGCTTTTTGTAGGTTGTGCTGTGGTT 476

146 MAY 2/ 10:20:41 2003

477 TITGGITGCTTCTCAGCTGCTGCCATGTTGGCAAGGCGCAGGGAGTACTTGTACCTCGGG 536

657 TACATCGTCTTTGACACCCAAGAAATTATT 686

597 GGTGGTTCCATGGCTGTTTTCAAGTTTGAGTTGTATTTTGGACTCTTGGTGTTTGTGGGC 656

297 GCTIGCATGGGAAGCATGGTGTGGCTTCTCTCAGCTCCTTATCAAGAGCAAAAAGG 356

357 GIGGCICTICTGATGGCAGCTGCACTTTTTGAAGGCGCCTCTATTGGTCCTCTGATTGAG 416

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447 TITGGCGCTTTTGTAGGTTGTGCTGTGTTTTTGGTTGCTTCTCAGCTGCTGCCATGTTG 506
                                                                                            979 higginaccchichreccchicheritariacccmidicalacticitatic
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3.6%; Score 36.8; DB 4; Length 601;
Best Local Similarity 51.4%; Pred. No. 0.53;
Matches 142; Conservative 0; Mismatches 122; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  859 GAGAAGTIACACTIGGGTAGAACCCTIGITGCCCTIGTCCTGGTTGTTGCCA 808
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Patent No. 6262334

GENERAL INCOPRATION:
TITLE OF INVENTION: WOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS: II
FILE REPERENCE: COUNA-260XX
CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT FILING DATE: 1999-08-30
EARLIER FILING DATE: 1999-06-08
EARLIER FILING DATE: 1999-06-08
EARLIER FILING DATE: 1999-01-27
EARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 544

SOFTWARE: FastSRQ for Windows Version 3.0

LENGTH: 601
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NAME/KEY: misc_feature

LOCATION: (1)...(601)

OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
US-09-385-982-231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318
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1803 CAGATCTTAACGTTTATGTTCAATCAACTTTTGGAGGCATTGACAGGTACGAAATTT 1744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGTTTATGATTAAGTTCAATCTTAGAATATGAATTTAACATCTATTATAGATGCATAAA 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       630 TATTTTGGACTCTTGGTGTTTGTGGGCTACATCGTCTTTGACACCCCAAGAAATTATTGAG 689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2169;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
3.3%; Score 34.6; DB 3; Length 2
Best Local Similarity 47.8%; Pred. No. 3.7;
Matches 100; Conservative 0; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TILE OF INVENTION: INHIBITION OF GENE EXPRESSION FILE REFERENCE: 674509-2004
CURRENT APPLICATION NUMBER: US/08/981,803
CURRENT PILING DATE: 1997-04-17
EARLIER APPLICATION NUMBER: PCT/EP96/03052
EARLIER FILING DATE: 1996-07-12
EARLIER FILING DATE: 1996-07-12
EARLIER FILING DATE: 1995-07-14
SERLIER FILING DATE: 1995-07-14
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3.3%; Score 34.6; DB 3;
Best Local Similarity 47.8%; Pred. No. 3.7;
Matches 100; Conservative 0; Mismatches 109;
                                     INHIBITION OF GENE EXPRESSION
APPLICANT: POULSEN, PETER
TITLE OF INVENTION: INHIBITION OF GENE EXPRESS
FILE REPERENCE: 674509-2004
CURRENT PEDELICATION NUMBER: US/08/981,803
CURRENT FILING DATE: 1997-04-17
BARLIER APPLICATION NUMBER: PCT/EP96/03052
BARLIER PILING DATE: 1996-07-12
BARLIER FILING DATE: 1995-07-14
SARLIER FILING DATE: 1995-07-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 14
LENGTH: 2169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              810 AAGAAGAAGAAGAGGAGAAACTAGATTTG 838
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US-08-981-803-28/c
; Sequence 28, Application US/08981803
; Patent No. 6147279
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA;
CRGANISM: Solanum tuberosum
US-08-981-803-14
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; ORGANISM: Solanum tuberosum
US-08-981-803-28
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RESULT 10
US-08-981-803-14
Seque 14, Application US/08981803
Facent No. 6147279
GENERAL INFORMATION:

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1803 cadarctraacertrarerrearcaacritricaacearicacaecracacacaaritr 1744
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                                                                                                   TATITIGGACICITIGGIGITITGIGGGCTACATCGICITIGACACCCAAGAAATTATIGAG 689
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DB 4; Length 2169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATE: POULSEN, PETER
TITLE OF INVENTION: INHEBITION OF GENE EXPRESSION
FILE REFERENCE: 674509-2004
CURRENT APPLICATION NUMBER: US/08/981,803
CURRENT FILING DATE: 1997-04-17
EARLIER APPLICATION NUMBER: PCT/EP96/03052
EARLIER FILING DATE: 1996-07-12
EARLIER FILING DATE: 1995-07-14
FARLIER FILING DATE: 1995-07-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
Score 34.6; DB 4; I
Pred. No. 3.7;
0; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34.6; DB 3;
Pred. No. 7.5;
0; Mismatches 109;
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Batent No. 6232122
GENERAL INFORMATION:
APPLICANT: POULSEN, Peter
TITLE OF INFUNITION: INHIBITION OF GENE EXPRESSION
FILE REFERENCE: 674509-2003
CURRENT APPLICATION NUMBER: US/08/983,440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1683 AATAGCTAATGATAGAACATTGACATTTG 1655
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US-08-981-803-29
'Sequence 29, Application US/08981803
'Patent No. 6147279
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Best Local Similarity 47.8%;
Matches 100; Conservative
  Query Match
Best Local Similarity 47.8%;
Matches 100; Conservative
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US-08-981-803-29
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US-08-983-440-29
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Pred. No. 3.7;
0; Mismatches 109; Indels 0
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TITLE OF INVENTION: INHIBITION OF GENE EXPRESSION
TITLE OF INVENTION: INHIBITION OF GENE EXPRESSION
CURRENT APPLICATION NUMBER: US/08/983,440
CURRENT FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 9514437.4
EARLIER PLING DATE: 1995-07-14
EARLIER PLING DATE: 1996-07-12
EARLIER FILING DATE: 1996-07-12
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PATENTIN Ver. 2.0
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TITLE OF INVENTION: INHIBITION OF GENE EXPRESSION
FILE REPERENCE: 674509-2003
CURRENT APPLICATION NUMBER: US/08/983,440
CURRENT FILING DATE: 1988-04-17
EARLIER APPLICATION NUMBER: 9514437.4
EARLIER FILING DATE: 1995-07-14
EARLIER FILING DATE: 1995-07-14
EARLIER FILING DATE: 1996-07-12
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PALCHIN Ver. 2.0
                                                                                                                                    1683 AATAGCTAATGATAGAACATTGACATTTG 1655
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                                                                                                                                                                                                                                                                Sequence 14, Application US/08983440 Patent No. 6232122
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Best Local Similarity 47.8%;
Matches 100; Conservative
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; ORGANISM: Solanum tuberosum
US-08-983-440-28
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; ORGANISM: Solanum tuberosum
US-08-983-440-14
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US-08-983-440-14
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Length 11478;

Indels

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Query Match 3.1%; Score 34.6; DB 4; Length 11478; Best Local Similarity 47.8%; Pred. No. 7.5; Matches 100; Conservative 0; Mismatches 109; Indels 0;
                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Solanum'tuberosum
PERTURE:
NAME/KEX: variation
NAME/KEX: variation
OTHER INFORMATION: B stands for G or C or T/U
PERTURE:
CURRENT FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 9514437.4
EARLIER FILING DATE: 1995-07-14
EARLIER FILING DATE: 1996-07-12
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PATENTING DATE: 1996-07-12
SOFTWARE: PATENTING DATE: 1996-07-12
LENGTH: 11478
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LOCATION: (1)..(11478)
OTHER INFORMATION: R stands for G or A
FERTURE:
NAME/KEY: variation
LOCATION: (1)..(11478)
OTHER INFORMATION: K stands for G or T/U
FEATURE:
NAME/KEY: variation
LOCATION: (1)..(11478)
OTHER INFORMATION: W stands for A or T/U
FEATURE:
NAME/KEY: variation
LOCATION: (1)..(11478)
OTHER INFORMATION: W stands for A or T/U
COATION: (1)..(11478)
OTHER INFORMATION: M stands for A or C
US-08-983-440-29
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810 AAGAAGAAGAGAGAGAAACTAGATTTG 838

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Search completed: May 25, 2003, 11:26:51 Job time : 90 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	Sequence 3, Appli	Sequence.15, Appl	Sequence 223, App	Sequence 17, Appl	Sequence 232, App	Sequence 31, Appl	Sequence 1, Appli	Seguence 33, Appl	Sequence 5, Appli	Sequence 3, Appli	Seguence 231, App	Sequence 43, Appl	Seguence 44, Appl	Seguence 7, Appli	Sequence 22, Appl	Sequence 1827, Ap	Sequence 19, Appl	Sequence 73; Appl	Sequence 356, App
SUMMARIES	ΩI	US-09-955-526-3	US-10-167-015-15	US-09-770-445-223	US-10-167-015-17	US-10-219-220-232	US-10-167-015-31	US-10-167-015-1	US-10-167-015-33	US-10-167-015-5	US-10-167-015-3	US-10-219-220-231	US-10-219-220-43	US-10-219-220-44	US-10-167-015-7	US-10-167-015-22	US-09-878-574-1827	US-10-167-015-19	US-09-925-302-73	US-10-044-090-356
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          CTGCTGGGGCTTACCTTCACATTCTATGGAATATCGGTGGCCTCCTCACAATGGCTT
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                              CTGCTGGGGCTTACCATTCTATGGAATATCGGTGGCCTCCTCACAATGGCTT
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Sequence 15. Application US/10167015
Publication No. US20030056249A1
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Johal, Gurmukh
APPLICANT: Acevedo, Pedro A. Navarro
APPLICANT: Tao, Yumin
TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
TCGTTCAAACTCATCTCAAGCAGGTGTACCTTACGCTATGC
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                                                                                                                                                                                                                                                                                   Length 735
                                                                                                                                                                                                                                                                             Query Match
41.5%; Score 429; DB 9; Length 73
Best Local Similarity 74.5%; Pred. No. 7.1e-124;
Matches 540; Conservative 0; Mismatches 185; Indels
AAACT 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   733
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                                                                                                                                                                                                                                                            612 GTTTTCAAGTTTGAGTTGTATTTTGGACTCTTGGTGTTTGTGGGCTACATCGTCTTTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17, Application US/10167015;
publication No. US20030056249A1
| GENERAL INFORMATION:
| APPLICANT: Simmons, Carl R.
| APPLICANT: Gordon-Kamm, William J.
| APPLICANT: Gordon-Kamm, William J.
| APPLICANT: Acevedo, Pedro A. Navarro
| APPLICANT: Tao, Yunin
| TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
| TITLE OF INVENTION: Thereof
| TITLE OF INVENTION: Thereof
| FILE REFERENCE: 1388
| CURRENT APPLICATION NUMBER: US/10/167,015
| CURRENT FILING DATE: 2002-66-11
| PRIOR APPLICATION NUMBER: 205-66-11
| PRIOR APPLICATION DATE: 2001-06-12
| NUMBER OF SEQ ID NOS: 34
| SOFTWARE: FastsEQ for Windows Version 3.0
| TEACH OF TABLES                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Pred. No. 3.8e-120;
0; Mismatches 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         792 GCATCTGAGAAGGAAGAAGAAGAAGAAGAGAAGAACT
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Best Local Similarity 74.4%;
Matches 526; Conservative C
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NAME/KEY: CDS

; LOCATION: (37)...(822)

US-10-167-015-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 AACCGCTGGAGTTATGATTCTCTCAAAACTTCCGCCAGATCTCACCTCTCGTTCAAACT 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           raccircargracicricadarardeseseraricararadacearragarenaraneseaer 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTGCTGCCATGTTGCCAAGGCGCAGGGAGTACTTGTACCTCGGGGGCCTTCTTTCATCT 551
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41.5%; Score 428.8; DB 10; Length 1009;
Best Local Similarity 73.7%; Pred. No. 1e-123;
Matches 560; Conservative 0; Mismatches 197; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SIAGE, TEST
APPLICANT: Davis, Keith R.
APPLICANT: Allen Keith R.
APPLICANT: Allen Keith R.
APPLICANT: Hoffman, Neith
APPLICANT: Hurban, Parrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE REPERBENGE: 2023US (PARA-012PRV)
CURRENT APPLICATION NUMBER: US 60/170,445
CURRENT FILING DATE: 2001-01-26
PRIOR PELICATION NUMBER: US 60/178,472
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOTTWARE: FastSEQ for Windows Version 4.0
                                                                                                                  Application US/09770445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page, Amy
Matthew, Abraham V.
Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA; ORGANISM: Arabidopsis thaliana
US-09-770-445-223
                                                                                                                                                                                                                                                                An, Yong-Qiang
Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
                                                                                                                                                                                                                                                                                                                                                                                                             Yu, Yang
Rameaka, Joshua G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           García, Carlos A.
Kricker, Maja
Slader, Ted
                                                                                                                                                 Patent No. US20020023281A1
GENERAL INFORMATION:
APPLICANT: Gorlach, Jorn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          252
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                                   790 ATGCATCTGAGAAGGAAGAAGAAGAAGAAGAGAGAA 828
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; LOCATION: (72)...(830)
US-10-167-015-31
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ORGANISM: Zea mays
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APPLICANT: Flind, Barry
APPLICANT: Landam, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of plant development
TITLE OF INVENTION: death and their use in the modification of plant development
TITLE OF INVENTION: 0.0022.0
CURRENT APPLICATION NUMBER: US.105/10/219,220
CURRENT FILING DATE: 2002-08-14
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 290
SOFTHARE FRASEO for Windows Version 3.0
SEQ ID NO 23: EALSEO for Windows Version 3.0
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) Sequence 232. Application US/10219220

; Publication No. US20030082724A1

; GENERAL INFORMATION:
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ORGANISM: Eucalyptus grandis
US-10-219-220-232
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Matches 519; Conservat
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Publication No. US20303056249A1

GENERAL INFORMATION:

APPLICANT: Simmons, Carl R.

APPLICANT: Gordon-Kamm, William J.

APPLICANT: Johal, Gurmukh

APPLICANT: Tao, Yumin

TITLE OF INVENTION: Thereof

FILE OF INVENTION: Thereof

FILE OF INVENTION: Thereof

FILE REPERBNCE: 138

CURRENT FILING DATE: 2002-06-11

FRIOR FILING DATE: 2001-06-12

NUMBER OF SEQ ID NOS: 34

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 31

LENGTH: 1026 30.4%; Score 314.4; DB 9; Length 65.9%; Pred. No. 7.8e-88; tive 0; Mismatches 236; Indels

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LENGTH: 1138
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No. 4.2e-87; Matches 466; Conservative 0; Mismatches 230; Indels
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Publication No. US20030056249A1

GENERAL INFORMATION:
APPLICANT: Simonons, Carl R.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Johal, Gurmukh Navarro
APPLICANT: Acevedo, Pedro A. Navarro
APPLICANT
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APPLICANT: Gordon-Kamm, William J.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Johal, Gurmukh
APPLICANT: Johal, Gurmukh
APPLICANT: Acvedo, Parmich
Tao, Yumin
TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
TITLE OF INVENTION: Thereof
FILE REFERENCE: 1388
CURRENT APPLICATION NUMBER: US/10/167,015
CURRENT FILING DATE: 2002-06-11
PRIOR FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 33
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Thereof

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FILE REFERENCE: 1388
CURRENT APPLICATION NUMBER: US/10/167,015
CURRENT FILING DATE: 2002-06-11
PRIOR APPLICATION NUMBER: US 60/297,478
PRIOR FILING DATE: 2001-06-12
SOTUMBER OF SEQ ID NOS: 34
SOTUMBER: FRREESQ for Windows Version 3.0
SEQ ID NO 5
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US-10-167-015-5
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Length 1139;
Query Match
30.0%; Score 310.4; DB 9;
Best Local Similarity 64.8%; Pred. No. 1.5e-86;
Matches 477; Conservative 0; Mismatches 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           813 AAGAAGAAGAGAAA 828
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Sequence 5, Application US/10167015
Publication No. US2030056249A1
GENERAL INFORMATION:
APPLICANT: Gimmons, Carl R.
APPLICANT: Johal, Gurmukh
APPLICANT: Acevedo, Pedro A. Navarro
APPLICANT: Acevedo, Pedro A. Navarro
APPLICANT: Tacevedo, Pedro A. Navarro
APPLICANT: Tace Yumin

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734 CCTITICACAGAITITGGCGCTGTTTTGTGCGGATTCTGATCATCATG-TTAAAGAATG 792
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; Publication No. US20030082724A1
; GENERAL INFORMATION:
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; ORGANISM: Pinus radiata
US-10-219-220-231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            494 TGCTGCCATGTTGGCAAGGCGCAGGGAGTACTTGTACCTCGGGGGCCCTTCTTTCATCTGG
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                                                                                                                                                                                                                                                                                                                               APPLICANT: Simmons, Carl R.
APPLICANT: Simmons, Carl R.
APPLICANT: Gorded-Kamm, William J.
APPLICANT: Gorded-Kamm, William J.
APPLICANT: Acevedo, Pedro A. Navarro
APPLICANT: Acevedo, Pedro A. Navarro
APPLICANT: Acevedo, Pedro A. Navarro
TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use;
TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use;
TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use;
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Pred. No. 6.9e-85;
0; Mismatches 235; Indels
                                                                                                                                                                        Sequence 3, Application US/10167015
Publication No. US20030056249A1
GENERAL INFORMATION:
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Best Local Similarity 65.9%;
Matches 457; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (72)...(830)
US-10-167-015-3
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ORGANISM: Zea mays
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APPLICANT: Internations affecting programmed cell
TITLE OF INVENTION: Compositions affecting programmed cell
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TITLE OF INVENTION: death and their use in the modification of plant development
TITLE OF INVENTION: 022c1
CURRENT APPLICATION NUMBER: US/10/219,220
CURRENT FILING DATE: 2002-08-14
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 290
SEQ ID NOS: 290
SEQ ID NO 231
LENGTH::102
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23.8%; Score 245.6; DB 9; Length
Best Local Similarity 60.6%; Pred. No. 3.1e-66;
Matches 423; Conservative 0; Mismatches 269; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 44, Application US/10219220
; Publication No. US20030082724A1
; GENERAL INFORMATION:
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) ORGANISM: Pinus radiata

US-10-219-220-44
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US-10-219-220-44
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US-10-167-015-7
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APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of plant development
FILE REPERENCE: 11000.1022a1 2012-08-14
PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 290
SOFFWARE: FastSEQ for Windows Version 3.0
SOFFWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 GGTGTACCTTACGCTATGCTGTGTGGCATCGGCTGGGGGCTTACCTTCACAT 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 TCTGTTGAATATTGGAGGGCTCCTCACGGGGCTCGCTTGCATTGGTTCTGTAATCGGGCT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 CTTATCCGTCCCTACTTCCTCGAACAATGAGGGTAAGAGAGCTGCGCTGCTGCTGGCAGC 183
694 CACACAGATGATCATCGAGAAAGCGGACCATGGAGACTATGATTATAAAACATTCACT 753
                                                                                                                                                        754 gaacererrearreaerregregregrarrierregecreargerearagearahagaa 813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CICCCTICTICTICGETTGCACTTTGCATCTTCCATTTTTGGTGGTTCCATGGCTGTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 221.2; DB 9; Length 8
Pred. No. 1.2e-58;
0; Mismatches 243; Indels
                                                                                                                                                                                                                                         791 TGCATCTGAGAAGGAAGAAGAAGAAGAAGAGAGAGAA 828
                                                                                                                                                                                                                                                                                                            814 TGCAGACAGTAAATCCAGGAAGGGAAAAAGAAGAGAA 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 43, Application US/10219220 Publication No. US20030082724A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 60.6%;
Matches 383; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
US-10-219-220-43
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APPLICANT: Film, Barry
APPLICANT: Film, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of plant development
TITLE OF INVENTION: death and their use in the modification of plant development
TITLE OF INVENTION: death and their use in the modification of plant development
CURRENT APPLICATION NUMBER: US/10/219,220
CURRENT PILING DATE: 2002-08-14
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 290
SEQ ID NOS: 290
SEQ ID NOS: 290
SEQ ID NO 44
LENGTH: 527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   441 ICGACCCGAGCATIGTGATAAGCGCATTTGTGGGATCTGCGCTGGCCTTCGCTTGTTTTTT 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTACCTTCACATTCTATGGAATATCGGTGGCCTCCTCACAACAATGGCTTGCATGGGAA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ciractecarcrearecreaacarcecegecrecreaceacarrecreerearearrecregaa 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      321 gcarcererecrecriricearricerecandaadakeaaaagagerridererek 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 GCAACCGCTGGAGTTATGATTCTCTCAAAACTTCCGCCAGATCTCACCTCTCGTTCAAA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 GCAAGGGGTGGAGCCACGATTCCCTCAAGAACTTCCGCCAGATATCTCCCGCCGTCCAAT 200
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737 TITCACAGAITITIGGCGCTGITITIGTGCGGAITCTGAICATCATGTTAAAGAAIGCAIC 796
                                                                       544 cricarreacricerrecreratricircecrearecrerratescaladareclas 603
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; Publication No. US20030056249A1
; General Information.
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Johal, Gurmukh
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT FILING DATE: 2002-06-11
; PRIOR FILING DATE: 2001-06-12
APPLICANT: Tao, Yumin
TITE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
TITE OF INVENTION: Thereof
FILE REPERENCE: 138
CURRENT FILING DATE: 2002-06-11
PRIOR APPLICATION NUMBER: US 60/297,478
PRIOR APPLICATION NUMBER: US 60/297,478
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PastSEQ for Windows Version 3.0
LENGTH: 740
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; LOCATION: (64)...(489)
US-10-167-015-7
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ORGANISM: zea mays
FEATURE:
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Best Local Simil
Matches 270; (
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GA 478
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US-10-167-015-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        692 GGCTCACTTGGGTGATATGGATTACGTTAAGCATGCATTGACCTTTTCACAGATTTTGG 751
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                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                               Length 308;
                                                                                                                                                                                                                                                                                               Query Match 17.2%; Score 177.8; DB 9; Length Best Local Similarity 75.6%; Pred. No. 2.4e-45; Matches 232; Conservative 0; Mismatches 74; Indels
NUMBER OF SEQ ID NOS: 34

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 22

LENGTH: 308

TYPE: DNA
ORGANISM: glycine max
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1) ... (308)

COTHER INFORMATION: n = A,T,C or G
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Job time : 170 secs
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BG134507 EST467399 BQ115430 EST600993 BP054243 EST439473 BI935239 EST555128

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A1895377 EST264820
BQ115431 EST660994
AN399756 EST710256
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BG641209 EST508828
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BG411594 AA11294
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A115692 BNLGH1671
A172192 BNLGH1671
A1731928 BNLGH1671
A1711928 BNLGH1671
A1711928 BNLGH1114
AY107681 Zea maye
BG46531 EST261431
A1711928 BNLGH1114
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Lycopersicon in diridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids I; Solanales, Solanaceae, Solanum,
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1 (bases 1 to 750)

van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Utterback,T.,
Hansen,C., Ronning,C. and Tanksley,S.
Generation of ESTS from tomato shoot/meristem tissue
Unpublished (2001)
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    .750
    /organism="Lycopersicon esculentum"
/cultivar="TA496"
    /db xref="taxon:4081"

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BU023368
BQ991270
BG646982
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BF635314
BG648573
BG647209
BQ401834
BQ165367
AI730983
AI726851
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BG124317.1 GI:12624505
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tomato.
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DEFINITION
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VERSION
KEYWORDS
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ORGANISM
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JOURNAL
COMMENT
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AUTHORS
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B1933489 EST553378
AW096641 EST289821
AW212279 EST304761
BG127849 EST40051
A1779122 EST260001
                                                                                                                           May 25, 2003, 09:52:48 ; Search time 1487 Seconds (without alignments) 11261.690 Million cell updates/sec
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                       GenCore version (c) 1993 - 2003
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Maximum Match 100%
Listing first 45 summaries
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AW096641
AW219279
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Score

Result Š.

Total number of

Database

Searched:

Title: Perfect score:

Sequence:

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Run on:

Scoring table:

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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids I; Solanales, Solanaceae, Solanum,
                                                                                                                                                                                                                                                                                                                                                                                                 van der Hoeven, R.S., Bezzerides, J.L., Karamycheva, S.A., Tsai, J., Vuterback, T., Van Aken, S., Roming, C.M., Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley, S.D. Generation of ESTs from tomato flower tissue, anthesis (2001) Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TACCTTCACATTCTATGGAATATCGGTGGCCTCCTCACAACAATGGCTTGCATGGGAAGC 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clemeon University Genomics Institute
Clemson University
100 'Oordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 13; Length 671;
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/cultivar="mio Grande PtoR"
/dultivar="mio Grande PtoR"
/done="clET39M"
/clone="clET39M"
/clone="clET39M"
/clone=lib="tomato mixed elicitor, BTI"
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/clone=lib="tomato"
/clon
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[ Lycopersicon.

] (Dasses 1 to 643)

D'Ascenzo, M., He.X., Lyman, J., Holt, I.E., Liang, F., Upton, J.,

B'Ascenzo, M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nierman, W.,

Ronning, C.M., Venter, J.C., Martin, G.B., Tanksley, S.D. and Giovannoni
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Eukaryota, Viridiplantee, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
Asteridae, euasterids I, Solanales, Solanaceae, Solanum;
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                                                                          GGCGTCTCCCCTTCTCTGGTTGCACTTTGCATCCTCCATTTTTGGTGGTTCCATGGCT
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                                      GATCCAAGCATTGTGTTTTGGCGCTTTTGTAGGTTGTGCTGTGGTTTTTTGGTTGCTTCTCA
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Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
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llarity 100.0%; Pred. No. 3.8e-154;
Conservative 0; Mismatches 0;
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AW219279 646 bp mRNA linear EST 18-MAY-2001 EST201761 tomato root during/after fruit set, Cornell University Lycopersicon esculentum cDNA clone cLEX3N8, mRNA sequence. AW219279
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van der Hoeven,R.S., Garvin,D., Matern,A.L., Holt,I.E., Liang,F.,
Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M.,
Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.
Generation of ESTs from tomato root tissue
Unpublished (1999)
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots,
Asteridae, euasterids I, Solanales, Solanaceae, Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
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GCAAACATAACATTGTCTACGTTCAGATAAATATCCTTTGCTCATTTCAGTTCCAAAAAC 62

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BG127849.1 GI:12628037
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/note="Vector: pBlueScript SK(-); Sire 1: Ecosh; Site 2: Indiana."
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAGCAAACATAACATTGTCTACGTTCAGATAAATATCCTTTGCTCATTTCAGTTCCAAAA 60
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                                                                                                                                                                                                                                                                                                                                                           Length 646;
                                                                                                                                                                                                                                                                                                                                                     Query Match
61.3%; Score 634; DB 10; Length 640
Best Local Similarity 99.8%; Pred. No. 7.8e-152;
Matches 645; Conservative 0; Mismatches 0; Indels
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/dev stage="developing shoots from 4-6wks old plants"
/lab_host="SOLR"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site 1: EcoR1; Site 2:
Xho1; Small expanding leaves from the growing tip were
taken from greenhouse plants (4-6wks old TA496). Tissue
was immediately frozen in liquid nitrogen."
154 c 153 g 211 t
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                                                                                                              Utterback, T.
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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                                                                                                                                                                                    Unpublished (2001)
Contact: CUGI
Clemson University
Clemson University
IO Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
                                             Lycopersicon.

1 (bases 1 to 647)

wan der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Utt Yansen,C., Ronning,C. and Tanksley,S.

Generation of ESTs from tomato shoot/meristem tissue
                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xraf="taxon:4081"
/clone="cTOF188"
/clone lib="tomato shoot/meristem"
/tissue_type="shoot/meristem"
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(bases 1 to 592)
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Contact: CUGI
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                                                                                                                     EST 18-MAY-2001
                                                                   596 bp mRNA linear EST 18-WAY-2001 clone cLES7M13, mRNA sequence.
A1779122 A1779122 A1779122.1 GI:5277163
                                                                                                                                                                                                                                     Lycopersicon esculentum
kukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
Asteridae, euasterids I, Solanales, Solanaceae, Solanum,
                                                                                                                                                                                                                                                                                                                                      D. Ascenzo, M., He, X., Lyman, J., Matern, A.L., Vision, T., Holt, I.E., Liang, F., Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nierman, W., Fraser, C.M., Venter, J.C., Tanksley, S.D., Giovannoni, J.J. and Martin, G.B. Generation of ESTs from Pseudomonas susceptible tomato Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        401 IGGICCICIGATICAGCIGGGCATIAACTICCAAGCATIGIGTITGGCGCTTTIGT 460
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/organism="Lycopersicon esculentum"
/cultivar="R11-13 (Rio Grande x Money Maker)"
/db xref="taxon:4081"
/clone="cleS7M13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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100.0%; Pred. No. 4.3e-142;
tive 0; Mismatches 0; Indels
 647
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/tissue_type="leaf"
/tissue_type="leaf"
/lab_host="SolR"
                    601 TTCCATGGGCTGTTTTCAAGTTTGAAGTTGTATTTTGGACTCTTGGTG
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Matches 596; Conservative
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                                                                                RESULT 6
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592 bp mRNA linear EST 31-JAN-2001
EST467399 tomato crown gall Lycopersicon esculentum cDNA clone
CTOEL6F5 5' sequence, mRNA sequence.
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/tissue_type="crown gall"
/dev_stage="crown galls from full-grown plants (8 wks old
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /nore="Vector: pBluescript SK(-); Site_1: EcoR1; Site_2: Xho1; Four wk old greenhouse plants were stab inoculated on stem with Agrobacterium tumefaciens C58 (Dr. T.J. Burr, Cornell U.). Galls were allowed to develop for another 4 wks, when gall tissue was frozen in liquid nitrogen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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301 AGGTIGIGCIGIGGTITITGGTIGCTICTCAGCTGCTGCCATGTIGGCAAGGCGCAGGGA
                                                                                                              GTACTIGITACTCGGGGGCCTTCTTTCATCTGGCGTCTCCCTTCTTCTGGTTGCACTT
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                                                               GTACTTGTACCTCGGGGGCCTTCTTTCATCTGGCGTCTCCCCTTCTCTTCTGGTTGCACTT
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
Location/Qualifiers
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Generation of ESTs from tomato crown gall tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Lycopersicon esculentum"
(diltyaz="TAX66"
|db xref="taxon:4081"
|clone="crosi6F5"
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Solanum tuberosum
Solanum tuberosum
Solanum: Solanales; Solanaceae; Solanum:
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
B. 1 (Abases II to 578)
Subell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C., Ratrepo, S., Griffiths, H., van der Hoeven, R., Tsai, J. and Karamycheva. S.A.
Generation of a set of potato cDNA clones for microarray analyses unpublished (2002)
On Apr 17, 2002 this sequence version replaced gi:20167379.
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, ND 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BQ115430 ST600993 mixed potato tissues Solanum tuberosum cDNA clone STMDA93 5' end, mRNA sequence. BE0115430 BQ115430.2 GI:21916950 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: potato@tigr.org
This clone is available through the Research Genetics, contact the
Research Genetics for further information 1-800-711-6195 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         542
                                                                                                                                                                                                                                                                                                                                                          CITCIGATGGCAGCTGCACTITITAAAGGGGCCTCTATIGGTCCTCTGATTGAGCTGGGC 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421 ATTAACTICGAICCAAGCAITGIGITIGGGGGCTTTIGIAGGIIGGGGGTTTTIGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           483 TGCTTCTCAGCTGCTGCCATGTTGGCAAGGCGCAGGAGTACTTGTACCTCGGGGGCCTT
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                    121 gecreredeaacegeregagriardarrerereaaaacrreegecagarereaere
                                                                                                                                                     TCGAAGAAGAAGAAGAACAATGGAAGGTTTCACATCGTTCTTCGACTCGCAATCT
                                                               GCCTCTCGCAACCGCTGGAGTTATGATTCTCTCAAAAACTTCCGCCAGATCTCACTCTC
                                                                                                                                   GITCAAACTCATCTCAAGCAGGTGTACCTTACGCTATGCTGTTTAGTGGCATCGGCT
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1. 578
/ Organism="Solanum tuberosum"
/cultivar="Kennebec or Binjte"
/db_xref="taxon:4113"
/clone="STMDA93"
/clone lib="mixed potato tissues"
/tissue_type="mixed tissues"
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BF054243 EST439473 potato leaves and petioles Solanum tuberosum cDNA clone eST339821 5' sequence, mRNA sequence.
BF054243 GI:10808139
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van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J., Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E., Tankeley, S.D. and Baker, B.
Unpublished (2000)
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; supplier: Combination of untreated and Phytophthora infestans-treated libraries of stolons, leaves, leaflets, axillary buds of stem explants, petioles, germinating eyes tubers, or roots."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251 TIACCTICACATICIATGGAATATCGGTGGCCTCCTCACAACAATGGCTTGCATGGGAAG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 GAAGAAGAAGAAGAATGGAAGGTTTCACATCGTTTCGACTCGCAATCTGCCTCTCG 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 TCATCTCAAGCAGGTCTACCTGACGCTATGCTGTGCTTTAGTGGCATCAGCTGCTGAGC
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                                                                                                                                                                                                                                                                         5,
                                                                                                                                                                                                                  Query Match 51.7%; Score 534.2; DB 14; Length 578; Best Local Similarity 96.5%; Pred. No. 3e-126; Matches 557; Conservative 0; Mismatches 18; Indels 2;
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Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="flower"
/dev stage="anthesis"
/dov stage="anthesis"
/note="vector: pBlusscript SK(-); Site_1: EcoRI; Site_2:
Xhol; supplier: Cornell University; sequencing: The
Institute for Genomic Research; Flower buds and flowers
were taken from greenhouse plants (4-8 wks old, TA496).
They were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
                                                                                                                      1 (bases 1 to 476)
van der Hoeven, R.S., Bezzerides, J.L., Karamycheva, S.A., Tsai, J.,
Utterback, T., Van Aken, S., Ronning, C.M., Nierman, W., Fraser, C.M.,
Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.
Generation of ESTs from tomato flower tissue, anthesis (2001)
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                       Genomics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGCTGGGCCTTACCTTCACATTCTATGGAATATCGGTGGCCTCCTCACAACAATGGCTTG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTTCTGATGGCAGCTGCACTTTTTGAAGGGCGCCTCTATTGGTCCTCTGATTGAGCTGGG 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGCCTCTCGCAACCGCTGGAGTTATGATTCTCTCAAAAACTTCCGCCAGATCTCAGCTCT 181
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  Lycopersicon esculentum
Sukaryoca, Viridiplantee, Streptophyta; Embryophyta; Tracheo
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae, euasterids I; Solanales; Solanaceae; Solanum;
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                                                                                                                                                                                                                                                                                                            Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
his clone is available through the Clemson University
Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Length 476;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone_lib="tomato flower, anthesis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Lycopersicon esculentum"
/cultiva="TA496"
/db_xref="taxon:4081"
/clone="cT0D22C8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.3%; Score 468.8; DB 13;
99.6%; Pred. No. 1.7e-109;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                   Contact: CUGI
Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Matches 470; Conservative
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                                                                                                    Lycopersicon.
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                                                                                                                         REFERENCE
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                                                                                                                                                                                                                                                                                                                                /note="Vector: pBlueScript SK(-); Site 1: EcoR1; Site 2: Xho1; Tissue was supplied by Dr. Fry (Cornell University). Leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in
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B1935239.1 G1:16249711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 CAACCGCTGGAGTTATGATTCTCTCTAAAACTTCCGCCAGATCTCACCTCTCGTTCAAAC 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 GGCAGCTGCACTTTTTTGAAGGCGCTTCTATTGGTCCTCGATTGAGCTGGGCATTAACTT 420
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                                                       Libraries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 12; Length 540;
Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics, I
Division tel 1-800-711-6195, email cdna@resgen.com
Location/Qualifiers
                                                                                                                   1. :540
/organism="Solanum tuberosum"
/cultivar="Kennebec"
/cultivar="taxon:4113"
/clone="cSTB39K21"
/clone lib="potato leaves and petioles"
/tissue_type="leaflets and petioles"
/dev stage="8 weeks old plants"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 498.4; DB 12; Length
Pred. No. 4.5e-117;
0; Mismatches 16; Indels
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Best Local Similarity 96.5%;
Matches 521; Conservative
                                                                                                                           Source
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AUTHORS
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JOURNAL
COMMENT
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                      ALSYSS77 464 bp mRNA linear EST 18-MAY-2001 EST264820 tomato callus, TAMU Lycopersicon esculentum cDNA clone alsorer.
                                                                                                                                                                                                                                        Lycopersicon.

Lycopersicon.

Alcala,J., Vision,T., Holt,I.E.

Alcala,F., Upcon,J., Craven,M.B., Bowman,C.L., Ahn,S., Ronning

C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.

Generation of ESTs from tomato callus tissue

Contact: CUGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone-libe-broad callus, TAMU"

tissue type="callus"

(dev_stage="25-40 dmRF""

/lab_host="X1-Blue MRF""

/note="Vector: pBlueScript SK(-); Site_l: EcoRl; Site_2:

Xhol; supplier: Giovannon! laboratory; CLEC - Cotyledons

of seedlings 7-10 days post-germination were excised, cut

at both ends and placed on MS medium with no selection.

Mixed callus was harvested at 25 and 40 days and included

undifferentiated masses. Tomato Callus EST Library"

a 112 c 116 g 137 t
                                                                                                                                                                     Lycopersicon esculentum
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids I, Solanales, Solanaceae, Solanum,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 IGCTGGGGCTTACCTTCACATTCTATGGAATATCGGTGGCCTCCTCACAATGGCTTG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       302 CATGGGAAGCATGGTGTGGCTTCTCTCTCTCTCTCTTATCAAGGGCAAAAAGGGTGGC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 TGCCTCTCGCAACCGCTGGAGTTATGATTCTCTCAAAAACTTCCGCCAGATCTCACCTCT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGCTGGGGCTTACCTTCACATTCTATGGAATATCGGTGGCCTCCTCACAACAATGGCTTG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCGAAGAAGAAGAAGAAGAACAATGGAAGGTTTCACATCGTTCTTCGACTCGCAATC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CTCGAAGAAGAAGAAGAGATCAATGGAAGGTTTCACATCGTTCTTCGACTCGCAATC 60
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                                                                                                                                                                                                                                                                                                                                                                                Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Lycopersicon esculentum"
|cultivax="TA46"
|db_xref="taxon:4081"
|clone="cLEC7H19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
43.9%; Score 454.4; DB 9;
Best Local Similarity 98.7%; Pred. No. 8.3e-106;
Matches 458; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        prime sequence.
Location/Qualifiers
                                                                                                                AI895377.1 GI:5601279
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                                                                                                                                                                                                                                   o mRNA linear EST 17-APR-2002
Solanum tuberosum cDNA clone STMDA93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: potato@tigr.org
This clone is available through the Research Genetics, contact the
Research Genetics for further information 1-800-711-6195 or
cha@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                         Solamum tuberosum

Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
I (bases: 1 to 617)
Buell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C.,
Restrepo, S., Griffiths, H., van der Hoeven, R., Tsai, J. and
Karamycheva, S.A.
Generation of a set of potato cDNA clones for microarray analyses
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   461 AGGITGIGCIGIGGITITITGGITGCITCTCAGCIGCTGCCATGTTGGCAAGGCGCAGGGA 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  557 Addingigenegininingeniecnichaecnechecandingedaadedaadeda 498
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361 CATTAACTTCGATCCAAGCATTGTGTTTGTGGCGCTTTTGTAAGTTGGGCTGTGGTTATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 25;
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Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
                                                                     525
                                                                                                          421 TIGCTICICAACTGCTGGCATGTTGGCAAGGCGCAGGGAGTACT 464
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Best Local Similarity 89.9%; Pred. No. 1.9e-104;
Matches 524; Conservative 0; Mismatches 34;
                                                                   482 TIGCIICICAGCIGCIGCCAIGIIGGCAAGGCGCAGGGAGIACI
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ESTG00994 mixed potato tissues S
3' end, mRNA sequence.
BQ15431
EQ115431
EST.
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RESULT 14
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Medrayota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids I; Solanales, Solanaceae, Solanum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 456)
D' Ascenzo,M., He,X., Lyman,J., Matern,A.L., Vision,T., Holt,I.B., Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W., Fraser,G.W., Venter,J.C., Tanksley,S.D., Glovannoni,J.J. and Martin,G.B.
Generation of ESTs from Pseudomonas resistant tomato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 456; ' 1987 18
                                                                           258
                                                                                                                                                                          197 GAGGAGAAACTAGATTTGGTTCTATGGGCTACTGGGACTCTAACCTGTGTGGTTTTCATA 138
                        377 cridendrinerescracarnercrineacacceaagaarnaridadaaagcicacri 318
                                                                                                       861
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                                                                                                                                                                                                                                         83
                                                                                                                                                          GAGGAGAAACTAGATTTGCTTCT--------CAACTTGTGGTTTCCANA
                                                                                                                                                                                                                                137 ATACACTGTGTTCACCTGAAACAAGCATGTTAATAGTTTGAAACTAG-----CTTTAGCA
                                                                    CTTGGTGTTTGTGGGCTACATCGTCTTTGACACCCAAGAAATTATTGAGAAGGCTCACTT
                                                   GGGTGATATGGATTACGTTAAGCATGCATTGACCCTTTTCACAGATTTTGGCGCTGTTTT
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100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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Pred. No. 1.5e-101;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prime sequence.
Location/Qualifiers
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AI776541.1 GI:5274582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.3%;
Matches 450; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: CUGI
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AI776541
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AUTHORS
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JOURNAL
COMMENT
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EST310250 L. pennellii trichome, Cornell University Lycopersicon pennellii cDNA clone CLPT8N10 5', mRNA sequence.
AW399750
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B., Fujii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lycopersicon pennellii
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots;
Asteridae, euasterids I; Solanales; Solanaceae, Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. (bases 1 to 448)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Lakey,J., Holt,I.E. Alcala,J., Vrebalov,J., White,R., Manen,T.S., 'Dton,J., Ronning,C.M., Craven,M.B., Fujii, F., Hansen,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from wild tomato (Lycopersicon pennellii)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Lycopersicon pennellii"
/db_xref="taxon:28526"
/clone="chPT8N10"
/clone_lib="L. pennellii trichome, Cornell University"
/tissue_type="trichome"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Leaves of various stages were shaken in liquid
                                                                                                                                                                                                                           198
                                                                                                                                                                                                                                                                                                                                          258
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78
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                                           CTACGTICAGATAAATATCCTTTTGCTCTTTTCAGTTCCAAAAACTCGAAGAAGAAGAAGA
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CTACGTTCAGATAAATATCCTTTGCTCATTTCAGTTCCAAAAACTCGAAGAAGAAGAAGA
                                                                                                            AGAGAACAATGGAAGGTTTCACATCGTTCTTCGACTCGCAATCTGCCTCTCGCAACCGCT
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 438 AGCATTGTGTTTGGCGCTTTTGTAGGTTGTGCT 470
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/lab_host="SOLR"
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Query Match
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nitrogen, shearing off trichomes. This procedure yielded a mixture of cells highly enriched for trichomes, with minor contamination by other types of leaf cells."
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1 (bases 1 to 488)
van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J., Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E., Tanksley, S.D. and Baker, B.

Upublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE919556

SST402-0CT-20G

SST402325 potato leaves and petioles Solanum tuberosum cDNA clone cSTE1D22 5' sequence, mRNA sequence.

BE919556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Cathy Ronning
The Institute for Genomic Research
For clone request: please contact Research Genetics, Libraries
Division tel 1-800-11-6195, email cdna@resgen.com.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                          249
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                                                                                                                                                                                                                                                           70 AGAAGAAGAAGAACAATGGAAGGTTTCACATCGTTTCGACTCGCAATCTGCCTCTC 129
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0
                                                                                                             Length 448;
                                                                                                             Score 423; DB 10; Length 4
Pred. No. 9.3e-98;
0; Mismatches 15; Indels
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/cultivar="Kennebec"
/db_vref="taxon:4113"
/clone="cSTB1D22"
/clone_lib="potato leaves and petioles"
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Solanum tuberosum
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/tissue_type="leaflets and perioles"
/dev stage="6 weeks old plants"
/lab_host="SOLK"
/not="vector: pBlueScript SX(-); Site_1: EcoR1; Site_2:
/hool; Tissue was supplied by Dr. Fry (Cornell University).
Leaflets and petioles were isolated from 8 week old
greenhouse grown plants. The plants were watered and
fertilized freely. The tissue was immediately frozen in
liquid nitrogen."
.0 a 113 c 116 q 149 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 AAGCAAACATTGTGTACGTTCAGATAAATAGCCTGTGCTCGTTTCAGTTCCAAAAACTC- 72
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ش
                                                                                                                                                                                                                                                                                                                                                                                         Length 488;
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                                                                                                                                                                                                                                                                                                                                                                                         40.8%; Score 422; DB 12; 94.1%; Pred. No. 1.7e-97; iive 0; Mismatches 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 450; Conservative
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May 25, 2003, 11:25:24; Search time 62 Seconds (without alignments) 533.002 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                             1272
1 MEGFISFFDSQSASRNRWSY......LIIMLKNASEKEEKKKKRRN 248
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GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                      908470 segs, 133250620 residues
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Maximum Match 100%
Listing first 45 summaries
                                                             OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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                                                                                                                                                            Title:
Perfect.score:
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                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                          Searched:
                                                                                                Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Testis Enhanced Ge	Testis Enhanced Ge	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	Bovine mammary tis	Lung cancer associ	Bax inhibitor BI-1	Human ovarian anti
	DI		AAB65756	AAG19970	AAG19969	AAG19971	AAG54829	AAB87615	AAB58178	AAW73136	ABP42996
	DB	22	22	21	21	21	21	22	21	13	23
	Query re Match Length DB I	213	140	138	154	110	129	236	255	237	245
do	Query	54.1	39.3	39.2	39.2	38.9	38.7	38.6	38.0	37.5	26.1
	Score	688.5	499.5	498.5	498.5	495	492.5	491.5	483.5	477.5	331.5
	Result No.		8	m	ধ	5	6	7	60	6	10

Novel defender against cell death polynucleotide useful for modulating programmed cell death pathway and specific development pathways in

Novel human secret	Drosophila melanog	Drosophila melanog	Drosophila melanog	Mouse brown adipos	Human secreted pro	secre	Human adult testis	Human haemopoietic	Membrane-bound pro	Human DERP2 protei	Human PRO281 (UNQ2	Human polypeptide	Human Pro peptide	Human polypeptide	Human secreted pro	Human ovarian tumo	Human cancer assoc	sec	PAAAG12 po	ich i	Zea mays protein f	Drosophila melanog	Zea mays protein i	Drosophila melanog	tein	tein	Secreted protein 1	rein	s thali	is chali	Œ		Human polypeptide,	Human ORFX ORF1966
2 AAU30218	~	2 ABB579	~	1 AAB49311	1 AAG0375	2 AAB6449	0 AAW81998	1 AAY7913	1 AAY6663	1 AAY5943	0	3 ABP6181	3 ABG340	m	σ	0 AAY7662	AAB439	AAB6448	AAY832	AAY3731	AAG3336	ABB6018	:1 AAG33367	ABB6019	AAG333	AAG4472	AAY5965	AAG44	AAG52	21 AAG52200	AAG5219	21 AAY77122	AAM9350	AAB4220
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ALIGNMENTS

Cell death modulator, programmed cell death, PCD; apoptosis; Testis Enhanced Gene Transcript protein #1. (GENE-) GENESIS RES & DEV CORP LTD. (FLET-) FLETCHER CHALLENGE FORESTS LTD. AAB65755 standard; Protein; 213 AA 02-JUN-2000; 2000WO-NZ00086. 99US-0325932. 27-MAR-2001 (first entry) WPI; 2001-061724/07. N-PSDB; AAF44782. Flinn B, Lasham A; WO200075331-A1. forestry plant. Pinus radiata. 04-JUN-1999; 14-DEC-2000. AAB65755; AAB65755 ä

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The present invention relates to coding sequences (see AP44740-F44840 and AAF44843-F44844) and proteins (see AAB65714-B65814) involved in programmed cell death (PCD, apoptosis). The coding sequences and proteins of the present invention are useful for modulating a PCD or cell death pathway and various developmental pathways in a forestry plant, by stably incorporating one of the present coding sequences into the genome of the forestry plant, where he coding sequence provides a PCD pathway that is not present in a native form of the forestry plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                    61 WNIGGLLTTMACMGSMVWLLSAPPYQEQKRVALLMAAALFEGASIGPLIELGINFDPSIV 120
                                                                                                                                                                                                                                                                                                                                                           1 MEGFTSFFDSQSASRNRWSYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHIL
                                                                                                                                                                                             39.3%; Score 499.5; DB 22; Length 140; 66.2%; Pred. No. 5.8e-51; ive 14; Mismatches 26; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana protein fragment SEQ ID NO: 21975.
                                                                                                                                                                                                                                                                                                                                                                                                            121 FGAFVGCAVVFGCFSAAAMLARREYLYLGG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                             118 ISAFVGSALAFACFSGAA-----CWLGG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG19970 standard; Protein; 138 AA
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99US-0123180.,
99US-0123548.
99US-0125788.
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99US-0128234.
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                                                                                                                                                                                                                                   Matches 100; Conservative
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                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                               140 AA;
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23-APR-1999;
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                                                                           The present invention relates to coding sequences (see AAF44740-F44840 prod AAF4443-F44844) and proteins (see AAB65714-B65814) involved in programmed cell death (PCD; apottosis). The coding sequences and proteins of the present invention are useful for modulating a PCD or cell death pathway and various developmental pathways in a forestry plant, by stably incorporating one of the present coding sequences into the genome of the forestry plant, where the coding sequence provides a PCD pathway that is not present in a native form of the forestry plant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    156
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                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                        39 QVYLTLCCALVASAAGAYLHILWNIGGLLTTWACMGSMVWLLSAP--PYQEQKRVALLMA 96
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                                                                                                                                                                                                                                                                      Length 213;
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                                                                                                                                                                                                                                                                                                          41; Indels
                                                                                                                                                                                                                                                                    54.1%; Score 688.5; DB 22;
illarity 64.6%; Pred. No. 3.8e-73;
Conservative 31; Mismatches 41; I
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(FLET-) FLETCHER CHALLENGE FORESTS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LFIDFVAVFVRLMVIMAKNADSKSREGKKKRR
                                              Claim 22; Pages 81-82; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB65756 standard; Protein; 140 AA
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                                                                                                                                                                                                                                                                                             Local Similarity
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Matches 137;
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                                                                                                   1 MEGFISFEDSQSASRNRWSYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHIL 60
                                                                    Query Match 39.2%; Score 498.5; DB 21; Length 138; Best Local Similarity 70.5%; Pred. No. 7.5e-51; Matches 91; Conservative 21; Mismatches 16; Indels 1;
                                                                                                                                                                                                                   Arabidopsis thaliana protein fragment SEQ ID NO: 21974.
                                                                                                                                                                                  AAG19969 standard; Protein; 154 AA.
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990S-0123180.
990S-0125788.
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99US-0134256
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PR 23-VIL-1999 99US-0145218.

PR 24-VIL-1999 99US-0145218.

PR 27-VIL-1999 99US-0149913.

PR 27-VIL-1999 99US-0149913.

PR 27-VIL-1999 99US-0149913.

PR 02-AUG-1999 99US-0149913.

PR 02-AUG-1999 99US-0149913.

PR 02-AUG-1999 99US-0147204.

PR 02-AUG-1999 99US-0147204.

PR 02-AUG-1999 99US-0147302.

PR 02-AUG-1999 99US-0147301.

PR 02-AUG-1999 99US-0144913.

PR 12-AUG-1999 99US-0144913.

PR 12-AUG-1999 99US-0144913.

PR 12-AUG-1999 99US-014491.

PR 22-AUG-1999 99US-014664.

PR 22-AUG-1999 99US-01493.

PR 22-AUG-1999 99US-014664.

PR 22-AUG-1999 99US-015518.

PR 23-AUG-1999 99US-015518.

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                                                                                                                                                              DB 21; Length 154;
                                                                                                                 Query Match 39.2%; Score 498.5; DB 21; Length Best Local Similarity 70.5%; Pred. No. 8.6e-51; Matches 91; Conservative 21; Mismatches 16; Indels
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04-MAY-1999;
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22-0CT-1999;
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AAG19971
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US-0132863	99US-0134256. 99US-0134218. 99US-0134219.	US-0134221 US-0134370 US-0134768	US-0134941 US-0135124	US-0135353	US-0136021 US-0136021	US-0136782	US-0137222 US-0137528	US-0137502	US-0138094	US-0138540 US-0138847	US-0139119	US-0139452	US-0139492	US-0139455	US-0139456	US-0139458	US-0139459	US-0139461	US-0139462	US-0139750	US-0139763	005-0139895 005-0139895	US-0140353	OUS-0140354 OUS-0140695	US-014082	3US-0140993	OC-0141842	3US-0142154	OUS-0142390	9US-0142803	OUS-014297	9US-0143547 9US-0143624	9US-014400	9US-0144089 9US-014408	9US-014432	9US-0144333 9US-0144333	9US-014433	9US-014433	9US-014435	9US-014463	9US-014488	9US-014508	9US-014508	9US-014508	9US-014508	010410-006
-MAY-1999	11-MAY-1999; 14-MAY-1999; 14-MAY-1999;	-MAY-1999	-MAY-1999	-MAY-1999	-MAY-1999	-MAY-1999	2001-ND5-1	1999 1-MIT-1	- JUN-1999	2001-NDD-1	9661-NUL-	566T-NDC-5	2001-NUL-1	9661-NDD-8	3-JUN-1999	2 - NUV - 1999	3-JUN-1999	2 - NOD - 8	- NDD-1999	3-JUN-1995	8-1995-8	2-VIOL-1993	8-NUL-199	961-ND5-8	8-JUN-199	9-1-NDD-6	1-JUL-199	1-JUL-199	6-TUL-199	8-JUL-199	2-JUL-199	3-701-199	5-JUL-199	6-JUL-199 6-JUL-199	9-JUL-199	9-1-JUL-9	9-JUL-199	9-JUL-199	0-JUL-199	0-JUL-199	0-JUL-199 1-JUL-199	1-JUL-199	1-JUL-199	2-JUL-199 2-JUL-199	2-JUL-199	66 T - TOO - 7
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99US-0145218.
99US-0145224.
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                                                                                                                                                                                                                                                                                                                                                Protein identification, signal transduction pathway, metabolic pathway, hybridisation assay; genetic mapping, gene expression control; promoter; termination sequence.
                                                                                                                                                                    139 MLARRREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELYFGLLVFVGYIVFDTQE 198
                                                                                                                                                   Gaps
                                                                                                                                                                                1 MLARRREYLYLGGLISSGLSMLMWLQPASSIFGGSASIFKFELYFGLLIFVGYMVVDTQE 60
                                                                                                                                                   .;
0
                                                                                                                               Length 110;
                                                                                                                                                                                                        199 IIEKAHLGDMDYVKHALTLFTDFGAVFVRILLIMLKNASEKEEKKKKRRN 248
                                                                                                                                                                                                                   61 IIEKAHLGDMDYVKHSLTLFTDFVAVFVRLJIMLKNSADKEEKKKKRRN 110
                                                                                                                                                  5; Indels
                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana protein fragment SEQ ID NO: 70059.
                                                                                                                                Query Match
38.9%; Score 495; DB 21;
Best Local Similarity 86.4%; Pred. No. 1.4e-50;
Matches 95; Conservative 10; Mismatches 5;
                                                                                                                                                                                                                                                                           AAG54829 standard; Protein; 129 AA
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990S-0125788
990S-0126264
990S-0127462
990S-0128714
990S-0129845
990S-0129845
990S-0130449
990S-0130489
990S-0132485
990S-0132486
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                           990S-0161404
990S-0161405
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990S-0161360-
990S-0161920-
990S-0161992-
990S-0161993-
990S-0161993-
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99US-0123548
   99US-0160980
            99US-0160981
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 22-OCT-1999;
22-OCT-1999;
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28-OCT-1999;
28-OCT-1999;
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28-OCT-1999;
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25. MAR. 1999;
29. MAR. 1999;
01. APR. 1999;
06. APR. 1999;
16. APR. 1999;
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9904S-01455119.
9904S-01455119.
9904S-0146588.
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9904S-0147302.
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26-JUL-1999;
27-JUL-1999;
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28-JUL-1999;
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02-AUG-1999;
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13-AUG-1999;
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27-AUG-1999;
30-AUG-1999;
31-AUG-1999;
01-SEP-1999;
07-SEP-1999;
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22-SEP-1999;
23-SEP-1999;
24-SEP-1999;
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New polypeptides and polynucleotides encoding the polypeptides, which are expressed in bovine mammary gland tissue, useful for stimulating mammary gland growth or function, or inducing differentiation of milk producing cells
                                                                                                                                                                                                                                                        60 WNIGGILTTIGCIGTMIWLLSCPPYEHQKRLSLLFASAVLEGASVGPLIKVAIDVDPSIL 119
                                                                                                                                                                                                                                          WNIGGLLTTMACMGSWWILLSAPPYQEQKRVALLMAAALFEGASIGPLIELGINFDPSIV 120
                                                                                                                                                                                       1 MEGFTSFFDSQSASRNRWSYDSLKNFRQISPLVQTHLKQVYITLCCALVASAAGAYLHIL 60
                                                                                                                                                                 1; Gaps
                                                                                                                                                                                                      The present invention relates to proteins derived from bovine mammary gland cells. The invention is useful for stimulating bovine mammary gland cell growth and function, inhibiting the growth of various mammary gland cancer cells, inhibiting anglogenesis and vascularization of tumours, or modulating the growth of blood vessels in a mammal.
                                                                                                                                        DB 21; Length 129;
                                                                                                                                     Match
Local Similarity 71.4%; Score 492.5; DB 21; Length
Local Similarity 71.4%; Pred. No. 3.5e-50;
Les 90; Conservative 20; Mismatches 15; Indels
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(NZPA-) NEW ZEALAND PASTORAL AGRIC RES INST LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bovine mammary tissue derived protein #6.
                                                                                                                                                                                                                                                                                                                                                                                        AAB87615 standard; protein; 236 AA
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         9903-0161405.
9903-0161406.
9903-0161369.
9903-0161360.
9903-0161361.
9903-0161992.
9903-0161993.
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                                                                                                                                                                                                                                                                                                121 FGAFVG 126
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Matches
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236 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer associated proteins represented in AAB58106 - AAB58548. Lung cancer associated proteins and polynucleotide sequences, their agonists, and antagonists may have neuroprotective; cytostatic; cardioactive; and tagonists may have neuroprotective; cytostatic; cardioactive; and active; cytostatic; cardioactive; and active; cytostatic; cardioactive; muscular, reproductive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lung cancer associated gene sequences, referred to as lung cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as lung cancer -
                                                                                                                                                                                                                                     77 VWLLSAPPYQ---EQKRVALLMAAALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCF 134
                                                                                                                                                                                                                 SAAAMLARRREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELYFGLLVFVGYIVF 194
                                                                                            19 SYDSLKNPRQISPLVQTHLKQVYLTLCCALVASAAGAYLHILWNI--GGLLTTMACMGSM 76
38.6%; Score 491.5; DB 22; Length 236; 42.9%; Pred. No. 1e-49; ive 53; Mismatches 72; Indels 7;
                                                                                                                                                                                                                                                                                       DIQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILIIMLKNASEKEEKKKK 245
                                                                                                                                                                                                                                                                                                              Lung cancer associated polypeptide sequence SEQ ID 516.
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(ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-MAR-2000; 2000WO-US05918.
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                                    Conservative
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                     Similarity
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 Query Match
                   Best Local
Matches 9
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gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders. The proteins may also be used in the treatment of wounds and infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and peptide AAF86459 are used in the course of the invention for the identification and characterisation of the polynucleotide and protein
                                                                                                                                                                                                                                                                                                             247
                                                                                                                                                                                              63 I--GGILTTMACMGSMVWLLSAPPYQ--EQKRVALLMAAALFEGASIGPLIELGINFDPS 118
                                                                                                                                                                                                                    71 FIQAGLLSALGSLILMIWIMATPHSHETEQKRLGLLAGFAFLTGVGLGPALEFCIAVNPS 130
                                                                                                                                                                                                                                          119 IVFGAFVGCAVVFGCFSAAAMLARRREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFK 178
                                                                                                                             Gaps
                                                                                                                                                 62
                                                                                                                                                                       70
                                                                                                                                                                                                                                                       17 GTMNIFD-----RKINFDALLKFSHITPSTQQHLKKVYASFALCMFVAAAGAYVHMVTH
                                                                                                                                                                                                                                                                                                     GFTSFFDSQSASRNRWSYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHILWN
                                                                                                                                                                                                                                                                                       179 FELYFGLLVFVGYIVFDTQEITEKAHLGDMDYVKHALTLFTDFGAVFVRILLIMLKNASE
                                                                                                                            13;
                                                                                                      Length 255
                                                                                                                            Indels
                                                                                                      DB 21;
                                                                                                    Query Match
38.0%; Score 483.5; DB 21;
Best Local Similarity 41.1%; Pred. No. 1e-48;
Matches 102; Conservative 54; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bax inhibitor; BI-1; human; apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "transmembrane
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                                                                                                                                                                                                                                                                                                                                                                                                                    AAW73136 standard; Protein; 237 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-US05015.
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                                                                                 255 AA;
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                                                             sednences
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                                                                                 Sequence
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Human, ovarian antigen, ovary, ovarian, breast, cancer, tumour, ovarian cancer, breast cancer, tumour, reproductive system disorder, infertility, pregnancy disorder, anovulation, polycystic ovary Syndröne, PCOS, ovarian cyst, dysmenotrhoea, endocrine disorder, infection, inflammatory condition, immune disorder; blood disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human ovarian antigen HPDWT56, SEQ ID NO:4128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABP42996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
ABF42996
ID ABF42
XX
AC ABF42
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DDT 22-AU
XX
XX
DE Human
XX
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Human
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KW NOVATI
KW OVATI
KW INFER
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cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy, chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                            07-JUN-2000; 2000US-209467P.
                                                                                                                                                                                                                                                                  07-JUN-2001; 2001WO-US18569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                                  Birse CE, Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                           2002-147878/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABQ56073
                                                                                                                                                                                  WO200200677-A1
                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                           03-JAN-2002.
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           This is the amino acid sequence of an inhibitor protein, termed .

B1-1, of the pro-apoptotic protein Bax. Nucleic acids encoding
B1-1 (see AAVS9067) and B1-2 (see AAVS9068) were identified by
suppression of Bax-induced death of yeast cells transformed to
suppression of Bax-induced death of yeast cells transformed to
express human Bax. A human HepG2 cDNA library was used for library
containing. The invention provides vectors, optionally expression
or viral vectors, containing B1 nucleic acids, and host cells
containing these vectors. The nucleic acids encoding B1-1/B1-2 can
be used to increase expression of these proteins in cells, or
antisense molecules prepared from them used to decrease expression.
In these ways, cellular apoptotic activity may be modulated. The
B1s and peptides portions are useful to detect, e.g. another B1 or a
member of the Bc1-2 family in biological samples. They are
cespecially useful in assays to identify agents (e.g. organic
cespecially useful in assays to identify agents (e.g. organic
college or peptides; claimed) modulating the specific association
of B1-1/B1-2 with a second protein (e.g. a B1, an anti-B1 antibody
cor a Bc1-2 family protein (e.g. Bax) (claimed)) e.g. in screening
cor alellular apoptotic activity (claimed). Bax overexpression is
cellular apoptotic activity (claimed). Bax overexpression is
cellular apoptotic activity (claimed). Bax overexpression is
spinal cord injuéry Parkinson's disease and Alzhaimer's disease.
Antibodies raised against the B1s and peptides are also useful e.g.
to detect/quantify B1s in biological samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 VWLLSAPPYQ--EQKRVALLMAAALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26
                                                                                            Bax inhibitor proteins, BI-1 and BI-2 - useful e.g. to modulate cellular apoptotic activity or identify agents altering BI-1 or BI-2 binding which can modulate apoptotic activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHILWNI--GGLLTTMACMGSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 SPDALKKSHITPSTQQHLKKVYASFALCMFVAAAGAYVHMVTHFIQAGLLSALGSLILM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 SAAAMLARRREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELYFGLLVFVGYIVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.5%; Score 477.5; DB 1
42.2%; Pred. No. 4.8e-48;
ive 53; Mismatches 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP42996 standard; Protein; 245 AA
                                                                                                                                                                                      Claim 14; Fig 1; 80pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 42.29
                                       WPI; 1998-531519/45.
N-PSDB; AAV59067.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237 AA;
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The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABG\$4131-ABG\$6305), and also cencempasses polypeptides 90% identical and polymolecides 95% identical to the sequences of the invention. The invention additionally relates to correct and bost cells comprising human ovarian antigens and the use of ovarian antigens, and the use of ovarian antigens, and the use of ovarian antigens, and the use of ovarian antigens and polypeptides in diagnosing, treating, prognosing or preventing various ovarian antigens, and the use of sorders. Such conditions include ovarian cancer and breast cancer, and disorders (e.g., infertility, disorders of pregnancy, anovulation, clisorders, infertinity, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorshoea), endocrine disorders, infertions (e.g., chlamydia (e.g., mastitis, opphoritis and ovaginitis), immune disorders (e.g., congenital and acquired toxic of modulate ovarian antigen polypeptides and conformation of individuals and in screening for compounds which modulate ovarian antigen expression or activity. The polymucleotides may be used in screening for compounds and the invention. Other individuals and in forensic analysis, and the invention. Other individuals and in forensic analysis, and the invention, but was obtained in electronic format directly from Wipport of For Wint for percents of the printed specification, but was obtained in electronic format directly from Wipport for the privation of the polymories. 78; Indels 11; DB 23; Length 245; 26.1%; Score 331.5; DB 2 34.8%; Pred. No. 1.1e-30; ftp.wipo.int/pub/published_pct_sequences Mismatches Claim 11; SEQ ID No 4128; 2922pp; English. 46; Conservative Similarity Local Sim. 72; Query Match Matches 셤 ઠે

4; 63 I -- CGLLTTMACMGSMVWLLSAPPYQ -- EQKRVALLMAAALFEGASIGPLIELGINFDPS 118 FIQAGLISALGSLILMIWLWATPHSHETEQKRLGLLAGFAFLTGVCLGPALEFCIAVNPS 130 Gaps GFTSFFDSQSASRNRWSYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHILWN 62

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NI --GGILLTTMACMGSMVWLLSAPPYQ--EQKRV--ALLMAAALFEGASIGPLI---ELG 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                 ABB63069;
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ABB63069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
     119 IVFGAFVGCAVVFGCFSAAAMLARRREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFK 178
                        Human, vaccination, gene therapy, nutritional supplement,
stem cell proliferation, haematopoiesis, nerve tissue regeneration,
immune suppression, immune stimulation, anti-inflammatory, leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.5%; Score 324; DB 22; 35.0%; Pred. No. 9.8e-30; iive 51; Mismatches 88;
                                                                          179 FELYFGLLVFVGYIVFDTQEIIEKAHL 205
                                                                                               190 ANLYXGLVVMCGFAFLILNSLLKRPNM 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; Page 262; 765pp; English.
                                                                                                                                                                                                     AAU30218 standard; Protein; 277 AA.
                                                                                                                                                                                                                                                                                                              Novel human secreted protein #709.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0552929
2001US-0770160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-APR-2001; 2001WO-US08656
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                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 277 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200179449-A2
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26-JAN-2001;
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                                                                                                                                                                                                                                     AAU30218;
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AAU30218
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection reagent for detecting 1900 or more for elucidating cell signalling and cell-cell
: | | | | : : | | | | | | | | | | | | HIDAGILSALGSILIMIWIMATPHSHETEQKRIGTSILGFCIPYRKIGIGFALGSFVIA 130
                                                                                                                 170 FGGSMAVFKFELYFGLLVFVGYIVFDTQEIIBKAHLGDMDY-VKHALTLFTDFGAVFVRI 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                190 FWIPFWVFQANLYVGLVVMCGFVLFDTQLIIEKARQGDQDYNLWHCIDLFLDFITVF---
                                               113 INFDPSIVFGAFVGCA-VVFGCFSAAAMLARR-REYLYLGGLLSSGVSLL-FWLHFASSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila, developmental biology, cell signalling, insecticide, pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 15999; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 245;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster polypeptide SEQ ID NO 15999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.5%; Score 312; DB 22; 34.4%; Pred. No. 2.2e-28; ive 48; Mismatches 83;
                                                                                                                                                                                                            247 ----QKNSMKDPGPXMKKDKKKRRRN 268
                                                                                                                                                                                         229 LIIMLKNASE ----KEEKKKKRRN 248
                                                                                                                                                                                                                                                                                                                  Ą
                                                                                                                                                                                                                                                                                                                ABB63069 standard; Protein; 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid
genes from Drosophila and
interactions
                                                                                                                                                                                                                                                                                                                                                                                    26-MAR-2002 (first entry)
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Best Local Similarity 34.4<sup>3</sup>
Matches 77; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-656860/75.
N-PSDB; ABL07172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PEKE ) PE CORP NY
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13;

88; Indels 34;

3 GFTSFPDSQSASRNRWSYDSLKNFRQISPLV-QTHLKQVYLTLCCALVASAAGAYLHILM_61.

93; Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                      81 GKNYYTRLGMLYAFGFCSGQTLGPLLGYICSINPAIILSALTGTFVTFISLSLSALLABQ 140
                                                                                                -----KRVALLMAAALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCFSAAAMLARR 143
                                                                                   144 REYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELYFGLLVFVGYIVFDTQEIIEKA 203
            PLVQTHLKQVYLTLCCALVASAAGAYLHI - - LWNIGGLLTTMACMGSMVWLLSAPPYQEQ 88
                                                                                                                                                                                                                                                                                           Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.1%; Score 192; DB 22; Length 305; larity 25.7%; Pred. No. 5.2e-14; Conservative 49; Mismatches 87; Indels 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 747; 21pp + Sequence Listing; English.
                                                                                                                             204 HLGDMDYVKHALTLFTDFGAVFVRILLIMLKNASEKBEKKKKRR 247
                                                                                                                                           Drosophila melanogaster polypeptide SEQ ID NO 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myers EW;
                                                                                                                                                                                                        ABB57985 standard; Protein; 305 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PWD,
                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2000; 2000US-191637P,
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid genes from Drosophila and interactions -
                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ε.
                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-656860/75.
N-PSDB; ABL02088.
                                                                                                                                                                                                                                                                                                                                                                                                                                              (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      305 AA;
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                                                                                                                                                                                                                                                  26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
85 HATYAYFGASCGVTAASAVAFFQSDAMMALMTRSGWVASLVTLGLVMLSGSIAQGLEYQP 144
                                                                                                                               145 GFGAKQLAWLVHCAVL-GAVLAPMCLLG----GPILTKALLYTSGIVGALSTVAACAPSE 199
                                                                                                                                                                                                            145 EYLYLGGILSSGVSLLF-----WLHFASSIFGGSMAVFKFELYFGLLVFVGYIVFDTQ 197
                                                                                                                                                                                                                                               85 YOEOXRVALLMAAALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCFSAAAMLARRR 144
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                                                                                                                                                                                                                                                                                                                                                               198 EIIEKAHLGDM-----DYVKHALTLFTDFGAVFVRILLIMLKNASEKEEKKKKRRN 248
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Best Local Similarity 26.5%; Pred. No. 1.4e-11;
Matches 56; Conservative 46; Mismatches 77; Indels 32
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36 HLKQVYLTLCCALVASAAGAY-----LHILWNIGGLLTTMACM-----GSMVWLLSAPP 84

Best Local Similarity Matches 61; Conserv

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The present invention provides a method of diagnosing abnormal levels of growth hormone (GH) in brown adipose tissue, by assaying the levels of specific gene transcripts. The genes of interest are those encoding specific gene transcripts. The genes of interest are those encoding ubiquichly incomerate, neuroleukin, private kinase, haem oxygenase, ubiquitin/ribosomal fusion protein, alpha-enolase, proteasome theta adipocyte lipid binding protein, medium chain acyl-coA dehydrogenase, adipocyte lipid binding protein, michochondrial cytochrome B or any of the genes Ng-G119X2, Ng-119X5, Ng-119X5, Ng-119X5, Ng-119X6, Ng-119X6, Ng-119X6, This is useful for diagnosing abnormal levels of GH or predicting changes in brown adipose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosis of abnormal levels of growth hormone in brown adipose tissue is carried out by monitoring the transcriptional activity of one or more genes related to growth hormone activity -
                                                        192 VHCAIL-GAVIAPICFMG---GPILTRAALYTGGIV-GGLSTIAACAPSDKFLYMGGPLA 246
                                                                                                          155 SGVSLLF-----WLHFASSIFGGSMAVFKFELYFGLLVFVGYIVFDTQEIIEKAHL-- 205
                                                                                                                               247 IGLGVVFASSLASMILPPTTALGAG---LASMSLYGGLVLFSGFLLYDTQRMVRRAEVYP 303
132 CVLTAAAAAATFRSHRLLELASRGGILATIASLALVIGSGAVARSIEYQPGLGAKHLAWA 191
                                   95 MAAALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCFSAAAMLARRREYLYLGGLLS
                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse brown adipose tissue clone 42 protein.
                                                                                                                                                                                206 ----GDMDYVKHALTLFTDFGAVFVRILIIM 232
                                                                                                                                                                                                            304 QYSYTPYDPINASMSIYMDVLNIFIRIVTIL 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Growth hormone; brown adipose tissue.
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                                                                                                                                                                                                                                                                                                            AAB49311 standard; Protein; 346
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84; Indels 32;

42 LTLCCALVASAAGAYLHIL----W-NIGGLLTTWACMGSMVWLLSAPPYQEQKRVALLMA 96

ch 13.4%; Score 171; DB 21; Length 346; 1 Similarity 25.9%; Pred. No. 1.9e-11; 57; Conservative 47; Mismatches 84; Indels 3:

Query Match Best Local S

Matches

ò g 97 AALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCFSAAAMLARRREYLYLGGLLSSG 156

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157 VSLLFWLHFASSIFGGSM-----AVFKFELYFGLLVFVGYIVFDTQEIJEKAHLG 206
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Sequence 1, Appli
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Sequence 28, Appli
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Sequence 13, Appli
Sequence 14, Appli
Sequence 16, Appli
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1 MEGFISFFDSQSASRNRWSY......LIIMLKNASEKEEKKKKRRN 248
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US-09-149-476-493
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US-09-372-422A-28
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Sequence 87, Application US/09325932A

Patent No. 6451604

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of forestry plant devel
FILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325,932A

CURRENT PILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 206
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APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of forestry plant devel
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                                US-09-641-259B-2
US-07-959-943-11
US-09-372-422A-32
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US-09-568-480-22
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US-09-568-486-22
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US-09-325-932A-88
US-09-325-932A-88
Sequence 88, Application US/09325932A
Patent No. 6451604
GENERAL INFORMATION:
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Matches 137; Conservative
    TYPE: PRT
ORGANISM: Pinus radiata
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US-09-325-932A-87
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Best Local Similarity 42.2%; Pred. No. 3.8e-48;
Matches 98; Conservative 53; Mismatches 74; Indels 7/5; Šaps;
                                                                                                                                                                                                                                                                                                                                                                                                             61 WNIGGLITTMACMGSMVWLLSAPPYQEQKRVALLMAAALFEGASIGPLIELGINFDPSIV 120
                                                                                                                                                                                                                      Query Match
39.3%; Score 499.5; DB 4; Length 140;
Best Local Similarity 66.2%; Pred. No. 4.7e-51;
Matches 100; Consérvative 14; Mismatches 26; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                      1 MEGFTSFFDSQSASRNRWSYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHIL 60
                                                                                                                                                                                                                                                                                                                                 RESULT 3
US-08-818-514-3
US-08-818-514-3
Sequence 3, Application US/08818514
; Patent No. 5837838
; GRNERAI INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Xv. Qunli
I TILE OF INVENTION:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRANT APPLICATION DATA:
APPLICATION TOTA:
APPLICATION TOTA:
APPLICATION TOTA:
APPLICATION TOTA:
APPLICATION TOTA:
FILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 FGAFVGCAVVFGCFSAAAMLARREYLYLGG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 ISAFVGSALAFACFSGAA-----CWLGG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2446
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 237 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       United States
                                                                                                                        ; LENGTH: 140
; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-325-932A-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRECT: 43.0.
CITY: San Diego
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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                                                                                                  SEQ ID NO 88
LENGTH: 140
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77 VWLLSAPPYO--EQKRVALLMAAALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCF 134
                                                                                     135 SAAAMLARREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELYFGLLVFVGYIVF 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 37.5%; Score 477.5; DB 4; Length 237; Best Local Similarity 42.2%; Pred. No. 3.8e-48; Matches 98; Conservative 53; Mismatches 74; Indels 7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 VWLLSAPPYQ--EQKRVALLMAAALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 IWLMATPHSHETBOKKIGLLAGFAFLTGIGLGPALBFCIAVNPSILPTAFMGTAMIFTCF 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 SAAAMLARRREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELYFGLLVFVGYIVF 194
9 NFDALLKFSHITPSTQQHLKKVYASFALCMFVAAAGAYVHMVTHFIQAGLLSALGSLILM 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 SYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHILWNI--GGLLTTMACMGSM 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        195 DIQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILLIMLKNASEKEEKKKKR 246
                                                                                                                                                                                                                                                                                                          188 DIQLIIEKAEHGDQDYIWHCIDLFLDFIITVFRKLMMILAMN--EKDKKKEKK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-115-934A-3
; Sequence 3, Application US/09115934A
; Parent No. 6130317
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Xu, Qunli
; TITLE OF INVENTION: BAX Inhibitor Proteins
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores Lip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION.
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/818,514
FILING DATE: 14-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Caltryn A.
REGISTRATION NUMBER: 31,815
REPERENCE/DOCKET NUMBER: P-LJ 3209
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-901
TELEFAX: (619) 535-905
SEQUENCE CHARACTERISTICS:
TENANTH: 237 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 237 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        California
: United States
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LING DATE:
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                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cooke, Michael Paul
APPLICANT: Cooke, Michael Paul
APPLICANT: Cooke, Michael Paul
APPLICANT: Birenko, Oksana
TITLE OF INVENTION: No. 6451558èl Genes in the Control of Hematopoiesis
FILE REPERENCE: 4.30629ASYS
CURRENT APPLICATION NUMBER: US/09/362,123A
CURRENT FILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: 09/128,310
PRIOR FILING DATE: 1998-08-03
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 345
TANDER: 1345
TANDER: 1345
TANDER: 1345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 HSTYMYLAGSIGLTALSALAISRTPVLMNFMMRGSWVTIGVTFAAMVGAGMLVRSIPYDQ 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 Q---KRVALLMAAALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCFSAAAMLARRR 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 BYLYLGGLLSSGVSLLFWLHFASSIFGGSM------AVFKFELYFGLLVFVGYIVF 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86; Indels 38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 HLKQVYLTLCCALVASAAGAYLH--ILWNI---GGLLT---TWACMGSMVWLLSAPPYQE 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIQEIIEKAHLGDM-----DYVKHALTLFTDFGAVFVRILLIMLKNASEKE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        195 DIQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILIIMLKNASEKEEKKKKR 246
                                                 188 DIQLIIEKAEHGDQDYIWHCIDLFLDFITVFRKLMMILAMN--EKDKKKEKK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.0%; Score 165; DB 4; Length 345; 26.3%; Pred. No. 4.1e-11;
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Patent No. 642056

GENERAL INFORMATION: 186 Human Secreted proteins applicants Prosen et al. 71TLE OF INVENTION: 186 Human Secreted proteins FILE REFERENCE: PZ002P1

FILE REFERENCE: PZ002P1

CURRENT APPLICATION NUMBER: US/09/149,476

CURRENT FILING DATE: 1998-09-08

EARLIER APPLICATION NUMBER: PCT/US98(04493)

EARLIER PILING DATE: 1998-03-06

EARLIER FILING DATE: 1997-03-07

EARLIER FILING DATE: 1997-03-07

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040,334

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040,334

EARLIER FILING DATE: 1997-03-07

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Sequence 493, Application US/09149476
Patent No. 6420526
                                                                                                                                                                                                                                                                             Sequence 2, Application US/09362123A
Patent No. 6451558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 26.3
Matches 61, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                         RESULT 5
US-09-362-123A-2
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PLICATION NUMBER: 60/047,582
LING DATE: 1997-05-23
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                                                                                                                                                                                                                                                    FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLICATION NUMBER: 60/043,568
LING DATE: 1997-04-11
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ION NUMBER: 60/043,311
                                                                                                                                    FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,633
                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/047,500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/047,598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLICATION NUMBER: 60/047,596
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ION NUMBER: 60/
                                                                                                                                                                                           APPLICATION NUMBER: 60/
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/
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                                                                                                                                                                                                                                                                                                                                                         PLICATION NUMBER:
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ERRLIER APPLICATION NUMBER: 60/056, 893
ERRLIER PILLING DATE: 1997-08-22
ERRLIER PLILLING DATE: 1997-08-22
ERRLIER PLILLOND DATE: 1997-08-23
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145 EYLYLGGLLSSGVSLLFWLHFASSIFGGSM------AVFKFELYFGLLVFVGYIVF 194 13.0%; Score 165; DB 4; Length 346; 26.3%; Pred. No. 4.1e-11; ive 47; Mismatches 86; Indels 38; Gaps 125 HSTYMYLAGSIGLTALSALAISRTPVLMNFMMRĠSWVTIGVTFAAMVGAGMLVRSIPYDQ 184 88 Q---KRVALLMAAALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCFŞAAAMLARRR 144 36 HLKOVYLTLCCALVASAAGAYLH--ILWNI---GGLLT---TMACMGSMVWLLSAPPYQE 87 DIQEIIEKAHLGDM------DYVKHALTLFTDFGAVFVRILIIMLKNASEKE 240 APPLICANT: Dunas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE BOUGUELET, Lydie
TILE REFERENCE: GENSET.021A
CURRENT APPLICATION INDRER: US/09/247,155A
CURRENT APPLICATION NUMBER: US/09/247,155A
CURRENT APPLICATION NUMBER: (0/094,121
EARLIER APPLICATION NUMBER: 60/091,563
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-06-10
EARLIER FILING DATE: 1998-06-10
EARLIER APPLICATION NUMBER: 60/095,116
EARLIER APPLICATION NUMBER: 60/095,273
EARLIER APPLICATION NUMBER: 60/099,273 BARLIER FILING DATE: 1997-04-11
BARLIER FILING DATE: 1997-04-11
BARLIER FILING DATE: 1997-08-22
BARLIER FILING DATE: 1997-08-22
BARLIER APPLICATION NUMBER: 60/056,664
BARLIER APPLICATION NUMBER: 60/056,816
BARLIER FILING DATE: 1997-08-22
BARLIER PAPLICATION NUMBER: 60/056,805
BARLIER FILING DATE: 1997-08-22
BARLIER APPLICATION NUMBER: 60/056,807
BARLIER FILING DATE: 1997-08-22
BARLIER FILING DATE: 1997-08-22
BARLIER FILING DATE: 1997-09-05
BARLIER FILING DATE: 1997-06-05
BARLIER APPLICATION NUMBER: 60/051,669
BARLIER APPLICATION NUMBER: 60/061,060 Sequence 89, Application US/09247155A Patent No. 6312922 GENERAL INFORMATION: Query Match 13.0% Best Local Similarity 26.3% Matches 61; Conservative RESULT 7 US-09-247-155-89 195 294 ठ a ઠે g ò

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214 ALTLFIDFGAVFVRILLIM 232
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  TOPOLOGY: linear IMMEDIATE SOURCE: LIBRARY: Consensus CLONE: Consensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 VVFGCFSAAA-MLARRREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELY---- 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 TVF--FGLTVYTLOSKKDFSKFG----AGLFALLWILCLSGF-----LKFFLYSEIME 179
                                                                                                                                                                                                                                                                                            75; Gaps
                                                                                                                                                                                                                                                                                                                                      50 ASAAGAYLHI-----LWNIGGLLTTMACMGSMVWLLSAPPYQEQKRV-----ALLMA 96
                                                                                                                                                                                                                                                                                                                                                                                 21 SSVASATVHIRMAFLRKVYSILSLQVLLTTVTSTVFL----YFESVRTFVHESPÄLIL- 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 IVLAAAGALLFCGFIIYDTHSLMHK--LSPEEYVLAAISLYLDIINLFLHLL 229
                                                                                                                                                                                                                                               Ouery Match

8.8%; Score 112.5; DB 4; Length 238;
Best Local Similarity 23.3%; Pred. No. 3.7e-05;
Matches 54; Conservative 36; Mismatches 67; Indels 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08794216
Sequence 1, Application US/08794216
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Coleman, Roger
TITLE OF INVENTION: NOVEL PROLINE-RICH MEMBRANE PROTEIN
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: Ralo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTSEE for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/794,216
FILING DATE: Herewith
CLASSIFFCATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 15
FILING DATE: ATTORNEY J.
FESTSEE BILLINGS, LUGY J.
NAME: BILLINGS, LUGY J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
TELECOMMUNICATION NUMBER: 415,855-655
TELEBRAK: 415-845-4166
TELEBRAK: 415-845-4166
TELEBRAK: 500 CD OF TO NO. 1.
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SEQUENCE CHARACTERISTICS:
LENGTH: 311 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
NUMBER OF SEQ ID NOS: 182
SCPTWARE. Patent.pm
SEQ ID NO 89
LENGTH: 238
TYPE: PRT
ORGANISM: HOMO Sapiens
FEATURE:
                                                                                                                                                       ; NAME/KEY: SIGNAL
; LOCATION: -53..-1
US-09-247-155-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
US-08-794-216-1
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41 YLTLCCALVASAAGAYLHILWNIGGLLTTMACMGSMVWLLSAPPYQEQKRVALLMAAALF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 QYVYWLKM------LYAALGAICFTLFLAYDTQLVLGNRKHTISPEDYITG 288
                                                                                                                                                                                                                                                                                            148 YLILAC-----CQGPRRRFPWNILLTLFTFAMGFMTGTISS-MYQTK---AVIIAMIIT 198
                                                                                                                                                                                                                                                                                                                                                                                         101 EGASIGPLIELGINFDPSIVFGAFVGCAVVFGCFSAAMLARRREYLYLGGLLSSGV--- 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      199 AVVSISVTI---FCFQTKVDFTSCTGLFCVLGI-------VLLVTGIVTSIVLYF 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158 SLLFWLHFASSIFGGSMAVFKFELY--FGLLVFVGYIVFDTQBII--EKAHLGDMDYVKH 213
Query Match

8.6%; Score 109; DB 2; Length 311;
Best Local Similarity 24.6%; Pred. No. 0.00014;
Matches 49; Conservative 28; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NESOURY
Sequence 1, Application US/08749289
Feach No. 595501
Feach No. 595001
Feach No. 595
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ATTONEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUTMERS: 36,749
REFERENCE/DOCKET NUTMER: PF-0:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 516 amino acids
TYPE: amino acid
STRANDEDNESS: single
TYPE: Animo acid
                                                                                                                                                                             TYPE: PRT; CRGANISM: Zea mays
US-09-372-422A-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
US-08-794-216-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 LVRGHITKLRALLYVAAQLLASSLACIL-LRYLSGGWVTPVHALGAGI-----RPMQGLV 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153 MEVILTFSLLFVTYAMILDPRSQVRTIGPLLT-----GLIVGANSLAGGNFTGA 201
                                                                                                                                                                                                                                                                                                           82 APPYQEQKRVALLMAAALFEGASIGPLI-ELGINFDPSIVFGAFVGCAVVFGCFSAAAML 140
                                                                                                                                                                                                                                                                                                                                                  244 ASFYNTE---AVIMAVGITTAVCFTVVIFSMQTRYDFTSCMGVLLVSMVVLFIFAILCIF 300
                                                                                                                                                                                                                                                                                                                                                                                                                 141 ARRREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELYFGLLVFVGYIVFDTQEII 200
                                                                                                                                                                                                                                                                                                                                                                                                                                            301 IRNR-------ILBIVYAS--------LGALLFTCFLAVDTQLLL 330
                                                                                                                                              134 EGPPSYYDNQDFPATNWDDKSIR------QAFIRKVFLVILLQLSVTLSTVSVFTFV 184
                                                                                                                                                                                                                                                       185 AEVKĞFVRENVWTYYVSYAVFFISLIVLSCCGDFRRKHPWNLVALSVLTASLSYMVGMI- 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 LVQTHLKQV --YLTLCCALVASAAGAYLHILWNIGGLLFTWACMGSMVWLLSAPPYQEQK 89
                                                         Gaps
                                                                                                                                                                                                        50 ASAAG-----AY-----LHIL------WNIGGLLTTWACMGSMVWLLS 81
                                                         96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
7.6%; Score 96.5; DB 4; Length 257;
Best Local Similarity 24.1%; Pred. No. 0.0031;
Matches 40; Conservative 33; Mismatches 58; Indels 35
Query Match
8.4%; Score 107; DB 2; Length 369;
Best Local Similarity 20.8%; Pred. No. 0.0003;
Matches 57; Conservative 41; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 AMLARREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELYF 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Rudolf Jung
APPLICANT: Maize Aquaporins and Uses Thereof
TITLE REFERENCE: 0919
CURRENT APPLICATION NUMBER: US/09/372,422A
CURRENT PILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: US 60/098,692
PRIOR APPLICATION NUMBER: US 60/098,692
PRIOR APPLICATION NUMBER: US 60/098,692
SACFWARE: RatcseQ for Windows Version 3.0
SOFTWARE: RatcseQ for Windows Version 3.0
LENGTH: 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 30, Application US/09372422A

Sequence 30, Application US/09372422A

Patent No. 6313375

GENERAL INFORMATION:

APPLICANT: Rudolf June

APPLICANT: Francois Barrieu

TIPLE OF INVENTION: Maize Aquaporins and Uses Thereof

FILE REFERENCE: 0919
                                                                                                        2 EGFTSFFDSQSASRNRWSYDSLKNFRQISPLVQTHLKQVYLTLCCAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201 -- EKAHLGDMDYVKHALTLFTDFGAVFVRILIIM 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-09-372-422A-28
'Sequence 28, Application US/09372422A
'Patent No. 6313375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
US-09-372-422A-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202
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97 ---AALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCFSAAAMLARRREYLYLGGLL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 LDPRKLLPGA--GPLLT------GLLVGANSVAGAALSGASMNPARSF---GPAV 204
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  42 LTLCCALVASAAGAYLHILWNIGGLLITMACMGSM/WLLSAPPYQEQKRVALLMA---- 96
                                                                                                                                                                                                                                                                                                                                                                                     Indels 25;
                                                                                                                                                                                                                                                                                                                           Query Match 7.5%; Score 95.5; DB 4; Length 249; Best Local Similarity 25.3%; Fred. No. 0.0039; Matches 38; Conservative 22; Mismatches 65; Indels 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, 54pplication US/08794216;
Sequence 3, 54pplication US/08794216;
Patent No. 54843716
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Coleman, Roger
ITILE OF INVENTION: NOVEL PROLINE-RICH MEMBRANE PROTEIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compartible
COMPUTER: IBM Compartible
COMPUTER: IBM Compartible
COMPUTER: SYSTEM: DOS
SOFTWARE: FASISEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION WHEER: US/08/794,216
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: COMPARE:
FILING DATE: COMPARE:
CURRENT APPLICATION NUMBER: US/09/372,422A
CURRENT FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: US 60/098,692
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PASLSEQ for Windows Version 3.0
SEQ ID NO 30
LENGTH: 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 SSGVSLLFWLHFASSIFGGSMAVFKFELYF 183
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Best Local Similarity 21.4%; Pred. No. 0.014;
Matches 56; Conservative 48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              319 VFAALNLYTDIINIFLYILTII 340
                                                                                                                                                                                                                                                                                                                                                                                    211 VKHALTLFIDFGAVFVRILLIM 232
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Zea mays
US-09-372-422A-26
                                                                                                                                       61 WNIGGL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-09-372-422A-26
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                                                                                                                                                                                                                       61 WNIGGL------LITIMACMGSMVWLLSAPPYQEQKRVALLMAAALFEG 102
                                                                                                                                                                                                                                                              161 GEVKĞFVRANVWTYYVSYAIFFISLIVLSCCĞDF------RKKHPWNLVALSILT- 209
                                                                                                                                                                                                                                                                                                    103 ASIGPLIELGINF -- DPSIVFGAFVGCAVVFGCFSAAM-LARRREYLYLGGLLSSGVSL 159
                                                                                                                                                                                                                                                                                                                                   210 ISLSYMVGMIASFYNTEAVIMAVGITTAV---CFTVVIFSMQTRYDFTSCMGVLLVSVVV 266
                                                                                                                                                                                                                                                                                                                                                                                    160 LFWLHFASSIFGGSMAVF----KFELYF---GLLVFVGYIVFDTQEII--EKAHLGDMDY 210
                                                                                                   Gaps
                                                                                                                                       2 EGFTSFFDSQSASRNRWSYDSLKNFRQISPLVQTHLKQVYLTLCCAL-VASAAGAYLHIL 60
                                                                                                   63;
                                                              Length 516;
                                                          // Score 94.5; DB 2; Length 51
// Pred. No. 0.014;
48; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-14-289-3

Sequence 3, Application US/08749289

Sequence 3, Application US/08749289

Patent No. 5955301

APPLICANT: Bandman, Olga

APPLICANT: Coleman, Roger

ITLE OF INVENTION: NOVEL HUMAN GLUTAMATE-BINDING

TITLE OF INVENTION: PROTEIN

NUMBER OF SEQUENCES:

CORRESPONDENCE 3

CORRESPONDENCE ADDRESS:

ADDRESSE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEM VETAIN 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,289
FILING DATE: Filed Herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTELLING DATE:
PILLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REFERENCE/DOCKET NUMBER: 36,749
TELEPHONICATION INFORMATION:
TELEPHONE: (415) 855-0555
TELEPHONE: (415) 845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211 VKHALTLFTDFGAVFVRILLIM 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           319 VFAALNLYTDIINIFLYILTII 340
                                                          Query Match
Best Local Similarity 21.4%;
Matches 56; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Palo Alto
STATE: California
COUNTRY: USA
  ; CLONE: 238267
US-08-794-216-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-749-289-3
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DB 2; Length 516;

7.4%; Score 94.5;

Query Match

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14;
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                                                                     103 ASIGPLIELGINF--DPSIVFGAFVGCAVVFGCFSAAAM-LARRREYLYLGGLLSSGVSL 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 MYRGHITKLRAVLYVAAQLLASSAACVLLRFL--SGGMVTPVHALGRGI-----SPMGGL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89 KRVALLMAAALF------EGASIGPLIELGINFDPSIVFGAFVGC-AVVFGCFSA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 VMEVILTESILEVIYAMILDPRSQVRAIGPLLT------GLIVGANSLAGGNFTG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 AAMLARREYLYLGGLLSSGVSILFWLHFASSIFGGSMAVFKFELYFGLLVFVGYIVFDT 196
                                                                                                                         -----LITIMACMGSMVWLLSAPPYQEQKRVALLMAAALFEG 102
  63; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32 LVQTHLKQVYLTLCCA---LVASAAGAYLHILWNIGGLLTTMACMGSMVWLLSAPPYQEQ 88
                                          2 EGFTSFFDSQSASRNRWSYDSLKNFRQISPLVQTHLKQVYLTLCCAL-VASAAGAYLHIL 60
                                                                                                                                                           161 GEVKGFVRANVWTYYVSYAIFFISLIVLSCCGDF-----RKKHPWNLVALSILT-
                                                                                                                                                                                                                                                                                            160 LFWLHFASSIFGGSMAVF----KFELYF----GLLVFVGYIVFDTQEII---EKAHLGDMDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.4%; Score 94; DB 4; Length 272; ilarity 22.6%; Pred. No. 0.0067; Conservative 32; Mismatches 70; Indels
95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    199 ASMNPARS----FGPALATGDWTNHWVYWIGPLLGGPLAGFVYESLF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 QEIIEKAHLGDMDY------VKHALTLF 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 --LVOKMHEAAAQWGSLTTISPCVVAHASCLF 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-07-879-617A-12
Sequence 12, Application US/07879617A
Setent No. 5580775
GENERAL INFORMATION:
APPLICANT: Fremeau Jr., Robert T.
APPLICANT: Caron, Marc G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 VASAAGAYLHILWNIGGILTTWACWGSWVWLLSAPPYQEQKRVALLMAAALFEGASIGPL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----YLKPNWQKLLETGV----WVD 305
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APPLICANT: Blakely, Randy D.
TITLE OF INVENTION: A High Affinity L-Proline Transporter
NUMBER OF SEQUENCES:
13
CORRESPONDENCE ADDRESS:
ADDRESSE: Kilpatrick & Cody
STREFF: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 3009
COMPUTER READABLE FORM:
MEDIUM ITYPE: Floppy disk,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.8%; Score 87; DB 1; Length 607; 22.7%; Pred. No. 0.14; tive 29; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/879,617A

FILING DATE: 19920501

CLASSIFICATION: 435

ATTONENEY/AGENT INPORMATION:

NAME: Pabet, Patrea L.

REGISTRATION NUMBER: 31,284

RESTRENCE/DOCKET NUMBER: BMU109

TELEPHONE: 404-815-6508

TELEFAX: 404-815-6508

TELEF
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NAME/KEY: Active-site
LOCATION: 102..103
OTHER INFORMATION: /note= "Leucine zipper motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) NAME/KEY: Active-site
; LOCATION: 116.117
; OTHER INFORMATION: /note= "Leucine zipper motif"
US-07-879-617A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 109..110
OTHER INFORMATION: /note= "Leucine zipper motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Leucine zipper motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAGMENT TYPE: N-terminal ORIGINAL SOURCE: ORGANISM: Rattus TISSUE TYPE: Brain - serotonin transporter PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---FGAWRG--VVF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Active-site
LOCATION: 95..96
OTHER INFORMATION: /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 22.7%
Matches 55; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280 -----
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Sequence 2 Sequence 3
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Run on:

Searched:

Sequence:

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61 WNIGGLITTMACMGSMVWLLSAPPYQEQKRVALLMAAALFEGASIGPLIELGINFDPSIV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FGAFVGCAVVFGCFSAAAMLARRREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 LYFGLLVFVGYIVFDTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILIIMLKNASEKE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MEGFISFFDSQSASRNRWSYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHIL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/0995526
Publication No. US20030009785A1
GENERAL INFORMATION:
APPLICANT: Read.
TITLE OF INVENTION: of Using Same
FILE REFRENCE: P-LJ 4001988: US/09/955,526
CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US 09/661,014
PRIOR FILING DATE: 2000-09-13
NUMBER OF SEQ ID NOS: 7
SOFFWARE: FastSEQ for Mindows Version 4.0
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100.0%; Pred. No. 5.4e-115;
tive 0; Mismatches 0;
               US-09-991-181-2
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US-09-991-181-2
US-09-991-653-2
US-09-990-653-2
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US-09-990-653-2
US-09-990-181-2
US-09-990-181-2
US-09-990-171-2
US-09-990-171-2
US-09-991-175-2
US-09-991-172-2
US-09-991-172-2
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US-09-991-172-2
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US-09-990-181-2
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LENGTH: 248

TYPE: PRT

ORGANISM: Lycopersicon esculentum
US-09-955-526-4
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248; Conservative
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Query Match
Best Local S:
Matches 248
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Sequence 274, Appl
Sequence 32, Appl
Sequence 34, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 27, Appl
Sequence 87, Appl
Sequence 87, Appl
Sequence 88, Appl
Sequence 88, Appl
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                                                                                                                                                          May 25, 2003, 12:22:59 ; Search time 54 Seconds (without alignments) 455.460 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 20,
Sequence 2, A
                                                                                                                                                                                                                                                            US-09-955-526-4
1272
1 MEGFISFFDSQSASRNRWSY......LIIMLKUASEKEEKKKKRRN 248
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Sequence
Sequence
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1: /cgn2_6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW PUB.pep:*

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14: //cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.pep:*
                       GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-955-526-4
US-10-167-015-16
US-10-167-015-18
US-10-167-015-18
US-10-167-015-32
US-10-167-015-34
US-10-167-015-34
US-10-167-015-4
US-10-167-015-4
US-10-187-015-4
US-10-219-220-87
US-10-219-220-88
US-10-219-220-88
US-10-219-220-88
US-10-219-220-88
US-09-99-23-38-2
US-09-992-598-2
US-09-992-33A-2
US-09-992-33A-2
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US-09-999-333A-2
US-09-999-333A-2
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                   - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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63 GGFLTTLASIGSMVWLLSTPPVEEQKRLSLLMASALFQGASIGFLIDLAIAIDPSLIVSA 122
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                                                                                                                                                                                                                                                                                                                                                                                       61 WNIGGELTTMACMGSMVWILSAPPYQEQKRVALLMAAALFEGASIGPLIELGINFDPSIV 120
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                                                                                                                                                                                                                                                                                                              1 MDAFASLFQS---SGKGWSHDSLKNFRQISPAVQSHLKNVYLSLCCALMASAGGAYLHLM 57
                                                                                                                                                                                                                                                 1 MEGFTSFFDSQSASRNRWSYDSLKNFRQISPLVQTHLKOVYLTLCCALVASAAGAYLHIL 60
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US-10-167-015-18

is Sequence 18, Application US/10167015

j Sequence 18, Application US/10167015

j Publication No. US20030056249A1

igeneral information:
    APPLICANT: Simmons, Carl R.
    APPLICANT: Gordon-Kamm, William J.
    APPLICANT: Acceded, Pedro A. Navarro
    APPLICANT: Acceded Acced
                                                                                                       Query Match 75.7%; Score 963.5; DB 9; Length 247; Best Local Similarity 74.4%; Pred. No. 3.1e-95; Matches 186; Conservative 27; Mismatches 32; Indels 5;
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; ORGANISM: Eucalyptus grandis
US-10-219-220-274
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Best Local Similarity 73.3%
Matches 178; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Glycine max
US-10-167-015-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 --EKKKKRRN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238 KNEKKKKRRD 247
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US-10-219-220-274
US-10-219-220-274
; Sequence 274, Application US/10219220
; Publication No. US030330082724A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Flinn, Barry
APPLICANT: Liana, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: USD2-002-04
; CURRENT APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: PRISEQ for Windows Version 3.0
; SEQ ID NO 274
LENGTH: 247
; TYPE: PRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 FTSFFDSQSASRNRWSYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHILWNI 63
                                                                                                                                                                NEGULIA (167-015-16)
Sequence 16, Application US/10167015
Septiment Simmons, Carl R.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Acevedo, Pedro A. Navarro
APPLICANT: Acevedo, Pedro A. Navarro
APPLICANT: Acevedo, Pedro A. Navarro
FILE FERENCE: 1380
FILE REPERENCE: 1380
CURRENT APPLICATION NUMBER: US/10/167,015
CURRENT FILING DATE: 2001-06-12
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 16
LENGTH: 244
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 77.7%; Score 988; DB 9; Length 244; Best Local Similarity 75.5%; Fred. No. 1.3e-87; Matches 185; Conservative 32; Mismatches 24; Indels
                                      241 EKKKKKRRN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||||:
240 KKRRD 244
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121 EFDPSILVTAFVGTAIAFACFSCAAWVAKRREYLYLGGLLSSGLSILLMLQFAASIFGHQ 180
SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 34 LENGTH: 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 LKNAADKSEDKRRKRRS 257
                                                                                                                                         Query Match
Best Local Similarity 65.8%
Matches 169; Conservative
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; ORGANISM: Zea mays
US-10-167-015-6
                                                          TYPE: PRT
CORGANISM: Zea mays
US-10-167-015-34
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Matches 169;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 VFGAFVGCAVVFGCFSAAAMLARRREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 AFFSASSASAPYGYGAGGWSYDSLKNFRQITPAVQTHLKLVYLTLCAALASSAVGAYLHV 62
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; Sequence 34, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Acevedo, Pedro A. Navarro
; TITLE OF INVENTION: Thereof
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2002-06-11
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
                                                                                                                                 USEQUENCE 32, Application US/10167015

PUDIcation No. US20030056249A1

SEQUENCE 32, Application US/10167015

PUDIcation No. US20030056249A1

SEQUENCE INFORMATION:

APPLICANT: Simmons.

APPLICANT: Gordon-Kamm, William J.

APPLICANT: Gordon-Kamm, William J.

APPLICANT: Acevedo. Pedro A. Navarro

APPLICANT: Acevedo. Pedro A. Navarro

APPLICANT: Acevedo. Pedro A. Navarro

TITLE OF INVENTION: Thereof

TITLE OF INVENTION: Thereof

TITLE OF INVENTION: Thereof

FILE REFERENCE: 1388

CURRENT APPLICATION NUMBER: US 60/297,478

FRICH FILING DATE: 2001-06-12

MUMBER OF SEQ ID NOS: 34

SEQ ID NO 32

IENGTH: 252

TYPE: PRT

CORGANISM: Zea mays

US-10-167-015-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 69.5%; Score 884.5; DB 9. Best Local Similarity 66.4%; Pred. No. 1.3e-77; Matches 166; Conservative 36; Mismatches 41.
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          244 KKR 246
                                         243 KKR 245
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US-10-167-015-34
                                                                                                                        -10-167-015-32
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54 GAYLHILWNIGGLLTTWACWGSMVWLLSAPPYQEQKRVALLMAAALFEGASIGPLIELGI 113
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                                                                                                                                                                                                                                                                                                                                                                                                      61 GAYLHVVWNIGGMITWLGCVGSIAWLFSVPVYEERKRYWLLMAAALLEGASVGPLIKLAV 120
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                                                                                                                                                                                                                                                                                                                                                            114 NFDPSIVFGAFVGCAVVFGCFSAAAMLARRREYLYLGGLLSSGVSLLFWLHFASSIFG-G 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 SMAVFKFELYFGLLVFVGYIVFDTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILIIM 232
                                                                                                                                                                                                                                       54 GAYLHILWNIGGLLTTMACMGSMYWLLSAPPYQEQKRVALLMAAALFEGASIGPLIELGI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MEGFTSFFDSQSASR-----NRWSYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAA 53
                                                                                                                     1 MEGFTSFFDSQSASR-----NRWSYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/10167015;
Publication No. US20030056249A1
GENERAL INPORMATION:
APPLICANT: Simmons, Carl R.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Acevedo, Pedro A. Navarro
APPLICANT: Tao, Yumin
TILE OF INVENTION: Thereof
FILE REFERENCE: 1388
CURRENT APPLICATION Thereof
FILE REFERENCE: 1388
CURRENT APPLICATION NUMBER: US/10/167,015
CURRENT FILING DATE: 2002-06-11
PRIOR APPLICATION NUMBER: US 60/297,478
PRIOR FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastERD for Windows Version 3.0
SEQ ID NO 6
SEQ ID NO 6
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.1%; Score 878.5; DB 9; Length 285; 65.8%; Pred. No. 5.8e-77; ive 37; Mismatches 42; Indels 9;
69.1%; Score 878.5; DB 9; Length 258; 65.8%; Pred. No. 5:2e-77; Live 37; Mismatches 42; Indels 9
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CURRENT FILING DATE: 2002-06-11
PRIOR APPLICATION NUMBER: US 60/297,478
PRIOR FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 34
SEQ ID NOS: 700FWARE: FRANKSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 250
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Matches 153; Conservative
                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 64.8
Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Pinus radiata
                                                                                                                                                                                                            TYPE: PRT ; ORGANISM: Zea mays US-10-167-015-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 KKRR 247
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US-10-219-220-273
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                                      173 SMAVFKFELYFGLLVFVGYIVFDTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILIIM 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Publication No. US2030056249A1
GENERAL INFORMATION
APPLICANT: Simmons, Carl R.
APPLICANT: Johal, Gurmukh
APPLICANT: Tao, Yumin
ITILE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
TITLE OF INVENTION: Thereof
TITLE OF INVENTION: Thereof
TITLE OF INVENTION: Thereof
TITLE OF INVENTION: Thereof
TITLE OF UNCATION NUMBER: US/10/167,015
                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/10167015
; Sequence 4, Application US/10167015
; Publication No. US2030056249A1
; GENERAL INFORMATION:
    APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Tao, Yunin
    TITLE OF INVENTION: Thereof
    TITLE OF INVENTION: THE                                                                                                                                                             ||||::||::||:
241 LKNAADKSEDKRRRRS 257
                                                                                                                            233 LKNASEK-EEKKKKRRN 248
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243 VGGQEEEEE 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Zea mays
US-10-167-015-4
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US-10-167-015-4
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Sequence 273, Application US/10219220
Publication No. US20030082724A1
GENERAL INFORMATION:
APPLICANT: Labham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE APPLICATION: US-220
CURRENT APPLICATION NUMBER: US/10/219,220
CURRENT FILING DATE: 2002-08-14
FRIOR APPLICATION NUMBER: US. No. US20030082724A1 09/325,932
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 290
SEGTWARE FREE FREE FREE FOR Windows Version 3.0
SEQ ID NO 273
LENGTH: 255
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                                                                                                                                                                                                                                                                                                                                    186 LVFVGYIVPDTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILLIIMLKNASEK--EEKK 243
                                                                                                                                                                                                                                                                                                                                                                                                                                     57 LHILWNIGGLLTTWACMGSMVWLLSAP--PYQEQKRVALLMAAALFEGASIGPLIELGIN 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 FDPSIVEGAFVGCAVVFGCFSAAAMLARRREYLYLGGLLSSGVSLLFWLHFASSIFGGSM 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
                                                                                                                                   1 MEGFTSF----FDSQSASRNRWSYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAY
                                                                                                   11 QSASRNR---WSYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHILWNIGGLL
                                                                                                                                                                                                                                                                                                       126 GCAVVFGCFSAAAMLARREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELYFGL
                                                7;
61.8%; Score 786.5; DB 9; Length 250; 64.8%; Pred. No. 3.7e-68; tive 34; Mismatches 45; Indels 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 255;
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60.2%; Pred. No. 8.6e-67;
tive 39; Mismatches 55;
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61 WNIGGLLTTMACMGSMVWLLSAPPYQEQKRVALLMAAALFEGASIGPLIELGINFDPSIV 120
                                                                                                                                                                                                                                  S8 LNIGGLLTTIACIGSIVWLLSIPPHEEQKRFGLLMAAALFEGACIGFLEAAIKVDPSIV 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 GSMAVPKFELYFGLLVFVGYIVFDTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILII 231
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                                                                                                                                                      1 MEGFTSFFDSQSASRNRWSYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHIL 60
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 140;
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Patent No. US20020044941A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
FILLE OF INVENTION: Nucleic Acids, Froteins and Antibodies
FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
FILING DATE: 2000-03-08
                                                                              26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23; Indels
                                   39.3%; Score 499.5; DB 9;
66.2%; Pred. No. 9.1e-41;
tive 14; Mismatches 26;
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                                                                                                                                                                                                                                                                                           121 FGAFVGCAVVFGCFSAAMLARREYLYLGG 151
                                                                                                                                                                                                                                                                                                                                 118 ISAFVGSALAFACFSGAA-----CWLGG 140
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124 MLKNGADKSEDKKRKKRS 141
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                                        Query Match
Best Local Similarity 66.2<sup>3</sup>
Matches 100; Conservative
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; ORGANISM: zea mays
US-10-167-015-8
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US-09-925-302-516
US-10-219-220-88
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Sequence 88 Application US/10219220
Sublication No. US20030082724A1
Sublication No. US20030082724A1
Sublication No. US20030082724A1
APPLICANT: Flinn, Barry
APPLICANT: Flinn, Darry
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: Gath and their use in the modification of plant development FILE REFERENCE: 11000.102201
CURRENT APPLICATION NUMBER: US/10/219,220
CURRENT FILING DATE: 299-06-04
RIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 290
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO SEQ ID NOS: 290
SEQ ID NO SEQ ID NOS: 290
                                                                                                                                                                                                                                  Sequence 87, Application US/10219220

Sublication No. US20030082724A1

GENERAL INFORMATION:

APPLICANT: Flinn, Barry

APPLICANT: Lashar, Annette

TITLE OF INVENTION: Geath and their use in the modification of plant development

TITLE OF INVENTION: Geath and their use in the modification of plant development

FILE REFERENCE: 11000.102201

CURRENT FILING DATE: 2002-08-14

FRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932

FRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932

FRIOR PRIOR FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 290

SOFTWARE: FastSEQ for Mindows Version 3.0

SEQ ID NO 8
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                                          97 AALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCFSAAAMLARREYLYLGGLLSSG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 AAAFKGATLGPLIDAVINIDSSILVSAFVGTSLAFACFSAAAITARREYLFLGGLLGSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 VSLLFWLHFASSIFGGSMAVFKFELYFGLLVFVGYIVFDTQEIIEKAHLGDMDYVKHALT 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 AVFKFELYFGLLVFVGYLVFDTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILLIMLK 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.1%; Score 688.5; DB 9; Length 213; 64.6%; Pred. No. 8.8e-59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                217 LFIDFGAVFVRILIIMLKNA-SEKEEKKKKRR 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 64.6
Matches 137; Conservative
                                                                                                                                235 NA-SEKEEKKKKRR 247
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ORGANISM: Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Pinus radiata
US-10-219-220-87
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US-10-219-220-87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 I--GGLLTTMACMGSMVWLLSAPPYQ--EQKRVALLMAAALFEGASIGPLIELGINFDPS 118
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                                                                                                                                                                                                                                                                                                                                                    3 GFTSFFDSQSASRNRWSYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHILMW 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20, Application US/10167015

Sequence 20, Application US/10167015

Publication No. US20030056249A1

GENERAL INFORMATION:

APPLICANT: Simmons, Carl R.

APPLICANT: Gordon-Kamm, Milliam J.

APPLICANT: Johal, Gurmukh

APPLICANT: Tao, Yumin

TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use

TITLE OF INVENTION: Thereof

FILE REFERENCE: 1388

CURRENT APPLICATION NUMBER: US/10/167,015

CURRENT FILING DATE: 2002-06-11

FRIOR APPLICATION NUMBER: US/0105

CURRENT FILING DATE: 2001-06-12

FRIOR PRICE OF SEQ ID NOS: 34

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 20

LENGTH: 78

LENGTH: 78

LENGTH: 78
                                                                                                                                                                                                                                                Query Match 38.0%; Score 483.5; DB 10; Length 255; Best Local Similarity 41.1%; Pred. No. 6.5e-39; Matches 102; Conservative 54; Mismatches 79; Indels 13;
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PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 516
LENGTH: 255
TYPE: PRT
TYPE: PRT
COGGANISM: Homo sapiens
US-09-925-302-516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CAGANISM: glycine max
US-10-167-015-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239 KEEKKKKR 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |::||:|:
248 KDKKKEKK 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-10-167-015-20
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171 GGSMAVFKFELYFGLLVFVGYIVFDTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILI 230

8 B 8

Search completed: May 25, 2003, 12:31:16 Job time : 55 secs

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GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 25, 2003, 12:16:44; Search time 43 Seconds (without alignments) 554.450 Million cell updates/sec

US-09-955-526-4 1272 1 MEGFTSFFDSQSASRNRWSY......LIMLKNASEKEEKKKKRRN 248 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 283224 seqs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	tion	inhibitor-1 [i	protein - rat	hetical prote		stis	e membrane	e carrier/t		e glutamate			mem	l membrane	conserved hypothet	e transport	e membrane		ed hypothet	probable integral	otein - Esc	tical prote	l pro	rotein - hu	e glutamate	hypothetical prote	e glutamte	conserved hypothet	ed hypothet	_
	Description	Bax inh	TEGI pr		TEGT Dr	•	probable	probable	probable	probable	probable	hypothetical	probabl	integral	conserv	probable	probable	hypothe	conserved	probabl	ybhl protein	hypothetica	hypothetica	HWLF2 p	probable g	hypothe	probable	conserv	conserved	conserved
SUMMARIES	QI	T52449	S42069	E71445	A85197	I38334	A10628	D85624	F90760	807180	T41414	T34438	S63281	AE3484	E81729	E71467	AI0142	T48120	A75462	D81441	B64815	H90736	A85587	QQBEGS	S38835	H64489	A64141	G81014	D82210	H64634
	DB	7	~1	7	~	(3	7	7	N	N	N	N	~1	~	N	~	~	N	01	7	ч	0	N		~	~	ď	7	7	Н
	Length	247	236	261	262	237	219	219	219	219	266	342	297	245	238	238	236	239	231	231	234	234	234	239	222	422	220	227	223	230
d¥	Query		37.7		37.1	37.1	13.4	12.4	12.4	ς.	11.3	ä	11.2	٠.	ö	。	。	9.8				9.6			4.6	٠.	٠.	٠.	8.9	
	Score	m	479	472	472	471.5	170.5	157.5	157.5	157.5	4	•	143		130.5		128	124.5	124	123.5	N	122	122	121.5	a	120	114.5	114		112.5
	Result No.	Н	7	m	4	Ŋ	9	7	æ	O)	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	53

RESULT 2 842069 TGT protein - rat C.Species: Rattus norvegicus (Norway rat) C.Species: Rattus horvegicus (Norway rat)

probable membrane	hypothetical prote	hypothetical prote	conserved hypothet	hypothetical prote	ABC transporter (p	N-methyl-D-asparta	ABC transporter (p	hypothetical prote	hypothetical prote	transport permease	transport permease	hypothetical prote	hypothetical prote	conserved membrane	oligodendrocyte tr
AH0954	F71879	B97681	AI2905	H71724	AB1293	S53708	AH1664	AG1350	E97723	H86611	A72013	AB1721	T01080	D97248	JC7692
7	~	7	~	7	~	~	~	7	7	~	N	~1	~	7	0
232	230	260	260	236	629	203	670	225	236	238	238	225	248	231	511
ω ω	9.6	9.0	9.0	ю	ю Э	8.2		9.0	8.0	8.0	8.0	7.8	7.8	7.8	7.7
112	109.5	109	109	108.5	106	104	103.5	101.5	101.5	101.5	101.5	99.5	99.5	66	98.5
30	31	32	33	34	35	36	37	38	39	4,0	41	42	43	44	4.5

ALIGNMENTS

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Gaps

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A85197
TEGT protein homolog [imported] - Arabidopsis thaliana
TEGT protein homolog [imported] - Arabidopsis thaliana
(s)Species Arabidopsis thaliana (mouse-ear cress)
C)Species Arabidopsis thaliana (mouse-ear cress)
C)Accession: A85197
A; Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Colc Nature 402, 769-777, 1999
A; Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A; Reference number: A85001; MUID:20083488; PMID:10617198
A; Accession: A85107
A; Attacks: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-262 <STO>
A; Consorreferences: GB:NC_001268; NID:94455800; PIDN:CAB10538.2; GSPDB:GN00140
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Cipate: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 11-Jan-2000
Cipate: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 11-Jan-2000
Cipate: L.; Marynen, P.; Szpirer, J.; Levan, G.; Guenther, E.
Genomics 28, 301-304, 1995
A;Reference number: 138334; MUID:96015061; PMID:8530040
A;Reference number: 138334; MUID:96015061; PMID:8530040
A;Recession: 138334
A;Molecule type: mRNA
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-237 <RBS>
A;Cross-references: EMBL:X75861; NID:9456258; PIDN:CAA53472.1; PID:9458545
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 EOKRVALLMAAALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCFSAAAMLARRREY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 LYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELYFGLLVFVGYIVFDTQEIIBKAHLG 206
                                                                                                                                                                                                                                                                                                                            147 LYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELYFGLLVFVGYIVFDTQEIIEKAHLG 206
                                                                                                                                                                                                                                                                                                                                                                                   94 EAKRLYLLFLFALLKGASVGPMIMLVIDFDSSVLVTAFVGTAVAFVCFSAAAMLATRRBY 153
                                                                                                                                       87 EQKRVALLMAAALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCFSAAAMLARREY 146
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                                                       Indels
Pred. No. 1.9e-35;
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61.7%; Pred. No. 1.9e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 DMDYVQHSFTFFTDFASLFVQILVLNMLIILEKK 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DMDYVKHALTLFTDFGAVFVRILLIIMLKNASEKE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TEGT (testis enhanced gene transcript) - human
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A;Cross-references: GDB:378256; OMIM:600748
A;Map position: 12q12-12q13
C;Superfamily: human testicular protein TEGT
          Local Similarity 61.7%; Pr
nes 95; Conservative 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Best Local Similarity
Matches 95, Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Gene: d14825c
A,Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207
                                                  Matches
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                                                                                                                                                                                                                                 A)Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNB
A;Rosidues: 1-236 dGUE>
A;Cross-references: EMBL:X75855; NID:g456206; PIDN:CAA53470.1; PID:g456207
A;Cross-references: EMBL:X75855; NID:g456206; PIDN:CAA53470.1; PID:g456207
A;Reference number: 157015; MUD:94281747; PMID:B012111
A;Reference number: 157015; MUD:94281747; PMID:B012111
A;Reference number: 157015; MUD:94281747; PMID:B012111
A;Residues: 1-236 dRES>
A;Residues: 1-236 dRES>
A;Residues: 1-236 dRES>
A;Accession: 176675
A;Accession: 176675
A;Accession: 176675
A;Accession: 176675
A;Residues: 2-236 dRES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 SLSALYARRRSYLFLGGILMSAMSLMF-VSSLGNIFFGSIWLFQANLYMGLLVMCGFVJF 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Cross-references: EMBL:X75856; NID:g456208; PIDN:CAA53471.1; PID:g456209
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 VWILSAPPYQ - EQKRVALLMAAALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCF 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 SYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHILMNI --GGLLTTMACMGSM 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195 DIQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILIIMLKNASEKEEKKKKR 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 DIQLIIEKAEHGDKDYIWHCIDLFLDFVTLFRKIMLILAFN--EKDKKKEKK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 261;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
37.7%; Score 479; DB 2;
Best Local Similarity 43.1%; Pred. No. 3.9e-36;
Matches 100; Conservative 52; Mismatches 72.
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C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
                                                       R_iGuenther, E. submitted to the EMBL Data Library, January 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.1%; Score 472;
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C,Superfamily: human testicular protein TEGT
               S42069; I57015; I76675
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                                                                                                                                                 Reference number: S42069; Accession: S42069
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Query Match

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Gaps

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A;Accession: D85624
A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-219
A;Cross-references: GB:AE005174; NID:g12514158; PIDN:AAG55456.1; GSPDB:GN00145; UWGP:Z1
A;Experimental source: strain 0157:H7, substrain EDL933
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A,Experimental source: strain 0157:H7, substrain RIMD 0509952
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Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.4%; Score 157.5; DB 2; Length 219; 26.7%; Pred. No. 5.9e-07; ive 45; Mismatches 80; Indels 51
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les 64; Conservative
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A;Gene: ECs1054
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R;Parkhill, J; Dougan, G; James, K.D; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, H.T.; Connerton, P.; Cronin, A; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gacra, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Reference number: A80502; PMID:11677608
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A;Cross-references: GB:AL513382; PIDN:CAD08212.1; PID:g16502260; GSPDB:GN00176 C;Genetics:
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                                                                                                                Gaps
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                                                                                                          7;
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DB 2;
37.1%; Score 471.5; DB 2;
42.2%; Pred. No. 1.9e-35;
iive 51; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.4%; Score 170.5;
29.2%; Pred. No. 3.9e
Live 42; Mismatches
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C,Superfamily: Escherichia coli ybhi protein
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Best Local Similarity 29.24
Matches 66, Conservative
                                                                                                     98; Conservative
                                                        Similarity
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A;Molecule type: DNA
Query Match
Best Local S
Matches 98
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Notes States: 12191. 1718. Salandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D. Submitted to the EMBL Data Library, September 1998

Submitted to the EMBL Data Library, September 1998

A; Reference number: 221954

A; Reference number: 221954

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: DNA

A; Molecule type: DNA

A; Residues: 1-26 6 4000>

A; Cross-references: EMBL:AL031798; PIDN:CAA21183.1; GSPDB:GN00068; SPDB:SPCC576.04

A; Experimental source: strain 972h-; cosmid c576

A; Genetics: SPDB:SPCC576.04

A; Map position: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
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60
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C;Species: Caenorhabditis elegans
C;Bacession: T14438
R;Bradshaw, H.
B;Bradshaw, H.
B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IELGINFDPSIVFGAFVGCAVVFGCFSA--AAMLARREFYLYLGGLLSSGV-----SLL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 FWL----HFASSIFGGSMAVFKFELYFGLLVFVGYIVFDTQEIIEKAHLGDMDYVKHALT 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGVLGAVFAPLCFWA---GPVLTRAAWYTAGIV-GGLSATAITAPSEKFLMMSGPLAMGF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LWN------IGGLLTTMACMGSMVWLLSAPPYQEQKRVALLMAAALFEGASIGPL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 --FEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCFSAAAMLARRREYLYLGGLLSSGV 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 SQSASRNRWSYDSLKNFRQISPLVQ-----THLKQVYLTLCCAL-VASAAGA--YLHI 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 NESATEN----PAVDQFKNTTPVAECAKSIRMAFLRKVYAILTAQLFVTSLFGGIFYLHP 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.3%; Score 144; DB 2; Length 266; 24.9%; Pred. No. 1.2e-05; Indels iive 39; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 11.3%; Score 143.5; DB 2; Best Local Similarity 23.7%; Pred. No. 1.8e-05; Matches 51; Conservative 47; Mismatches 86;
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A;Map position: 4
A;Introns: 45/3; 67/1; 150/3; 186/1; 262/1; 314/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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          C; Accession: T41414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Matches 6
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T34438
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;Cross-references: GB:AE000199; GB:U00096; NID:g1787202; PIDN:AAC74056.1; PID:g1787205;
;Experimental source: strain K-12, substrain MG1655
;Genetics:
                                                                                                                                                                                                                                                                                    C; Species: Escherichia coli
C; Date: 07-580-1990 #sequence_revision 07-Sep-1990 #text_change 01-Mar-2002
C; Accession: S07180; #sequence_revision 07-Sep-1990 #text_change 01-Mar-2002
R; Tamura, F; Nishimura, S; Ohki, M.
B; Tamura, F; Nishimura, S; Ohki, M.
B; Tatile: The E. coli divE mutation, which differentially inhibits synthesis of certain A; Reference number: S07180; MUID:84236106; PMID:6376117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A/Status: translation not shown
A/Status: translation not shown
A/Status: translation not shown
A/Rolecule type: DNA
A/Ross-references: EMBL:X00547; NID:g41283; PIDN:CAA25218.1; PID:g41284
A/Experimental source: strain W3110
B/Statuser, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A/Title: The complete/genome sequence of Escherichia coli K-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable receptor-associated protein - fission yeast (Schizosacchardmydes bombe)
C,Species: Schizosaccharomyces pombe
C,Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 LTLVGMYGLMFL----TYKTANKPTGIISAFAFTGFLGYILGFILNTYLSAGMGDVIAMA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 LGGTALVFFCCS-AYVLTTRKDMSFLGGMLMAGIVVVLIGMVANIFLQLPALHLAIS--- 165
--AVF-----ILISSGAILFETSNII---HGGETNYIRATVSLYVSLYNIFVSLLSIL 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 GSMAVFKFELYFGLLVFVGYIVFDTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVKILII 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 219;
                                                                                                                                                                                                                                               probable glutamate receptor yccA - Escherichia coli (strain K-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Accession: A64838 facture: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title: The complete genome sequence of Escherichia coli K-12.; Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Superfamily: Bscherichia coli ybhi protein | Superfamily: Bscherichia coli ybhi protein | Superfamily: Bscherichia coli ybhi protein | Keywords: transmembrane #status predicted <TML> | 43-59 / Domain: transmembrane #status predicted <TM2> | 43-59 / Domain: transmembrane #status predicted <TM3> | 105-121 / Domain: transmembrane #status predicted <TM3> | 105-127 / Domain: transmembrane #status predicted <TM3> | 160-138 / Domain: transmembrane #status predicted <TM5> | 160-138 / Domain: transmembrane #status predicted <TM5> | 160-216 / Domain: transmembrane #status #status predicted <TM5> | 160-216 / Domain: transmembrane #status predicted <TM5> | 160-216 / Domain: transmembrane #status #status predicted <TM5> | 160-216 / Domain: transmembrane #status predicted <TM5> | 160-216 / Domain: transmembrane #status predicted
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12.4%; Score 157.5; DB 2
Best Local Similarity 27.0%; Pred. No. 5.9e-07;
Matches 65; Conservative 46; Mismatches 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecule type: DNA
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166
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Rised, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic, Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
                                                                                                             integral membrane protein [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Species: Brucella melitensis
C;Species: O1-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
C;Accession: AB3484
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Mazur, M.; Goltsman, B.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes Prittle: The genome sequence of the facultative intracellular pathogen Brucella meliter A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AE002287; GB:AE002160; NID:g7190237; PIDN:AAF39078.1; PID:g7190;
A;Experimental source: strain Nigg (MoPn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conserved hypothetical protein TC0206 [imported] - Chlamydia muridarum (strain Nigg) C;5pecies: Chlamydia muridarum, Chlamydia trachomatis MOPn C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Sep-2000 C;Accession: E81729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-245 «KUR»
A;Cross-references: GB:AE008917; PIDN:AAL53040.1; PID:g17983899; GSPDB:GN00190
A;Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 TIKRNISAMGSFLMMG---LFGLILASVVNIFLGSTALQFAISVIGVLIFAGLTAYDTQE 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 AYLHILWN---IGGLLTTWACMGSMVWLLSAPPYQE-----QKRVALLMA--AALF---- 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 -----LGGLLSSGVSLLFWLHFAS--SIFGGSMAVFKFELYFGLLVFVGYIVFDTQE 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29 SYMLGVYNWMAIGLAVTGLAAFGTAVLAQSNPAFQQLLFASPLRWVIMLAPLAAVFFLSF 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 YDSLKNFRQISPLVQTHLKQVX-----LTLCCALVASAAGAY--LHILWNIGGLLTT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 YD--RDYTQDSRLPGTFSSRVYGWMTAGLAVTALTSLGLYATGAYRTLFSLW----WVWC 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --PLIELGINFDPSIVFGAFVGCAVVFGCFSAAAMLARREYLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.7%; Score 136.5; DB 2; Length 245; 29.1%; Pred. No. 5.3e-05; ive 31; Mismatches 76; Indels 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199 IIEKAHLGD-----MDYVKHALTLFTDFGAVFVRILIIM 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202 | | : || : || | || || || || || || 202 IXEMYYEGDAADTQGRKIVMGALRLYLDFINMFMFLLQFM 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: Escherichia coli ybhi protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Superfamily: Escherichia coli ybhL protein
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Best Local Similarity 29.1%
Matches 64; Conservative
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Best Local Similarity
Matches 66; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                              A,Accession: AE3484
A,Status: preliminary
A,Molecule type: DNA
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A; Status: preliminary
A; Molecule type: DNA
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A;Map position:
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A;Residues: 1-297 <MAU>
A;Cross-references: EMBL:Z71581; NID:g1302402; PID:e239757; PID:g1302403; MIPS:YNL305c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fitle: Sequence analysis of a 30 kb DNA segment from yeast chromosome XIV carrying C, and a novel putative serine/threonine protein kinase gene. Reference number: S60394; MUID:96132033; PMID:8553702
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                                                                                                                                                                                                                                                                                              probable membrane protein YNL305c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein N0405
C;Species: Spaccharomyces cerevision
C;Date: 27-Apr-1996 #sequencervision
C;Accession: S63281; 860395; 86127
C;Accession: CT.C.; Urbanus, J.H.M.; Planta, R.J.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S63266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----VALLMAAALFEGA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 -IWLAVSPRPEDYEASVPEPLLTGSSEEPAQEQRRLPWYVLSSYKQKLTLLSIFTLSEAY 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 SIGPLIELGINFDPSIVFGAFVGCAVVFGCFSAAAMLARRREYLYLGGLLSSGVSLLFWL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HF----ASSIFGGSMAVFKFELYFGLL---VFVGYIVFDTQEIIEKAHLGDMDY 210
241 GVVFVANIGAFFLPPGSALGASLA-SIVVYGGLILFSAFLLYDTQRLVKKAENHPHSSQ 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecule type: DNA;
Residues: 1-297 <MAF>;
Crossreferences: EMBL:U23084; NID:g1050853; PID:g1050855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7:86-102/Domain: transmembrane #status predicted <TM1>
7:173-189/Domain: transmembrane #status predicted <TM2>
7:173-285/Domain: transmembrane #status predicted <TM3>
7:238-254/Domain: transmembrane #status predicted <TM3>
7:238-254/Domain: transmembrane #status predicted <TM5>
7:271-287/Domain: transmembrane #status predicted <TM5>
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                                                                                      -----HLGDMDYVKHALTLFTDFGAVFVRILLIM 232
                                                                                                                             | ::::| ::::| LYGSDMQIRSFDPINAQMSIYMDVLNIFMRLVMIM 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Experimental source: strain $288C
R;Maurer, K.C.T.; Urbanus, J.H.M.; Planta, R.J.
Yeast 11, 1303-1310, 1995
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A.Molecule type: DNA
A.Residues: 1-27,'0', «MANA
A.Cross-references: EMBL:U23084
R.Maurer, K.T.C.
Submitted to the EMBL Data Library, March 1995
A.Accession: S66127
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A)Status: preliminary
A)Molecule type: DNA
A)Residues: 1-238 <ARN>
A)Cross-references: GB:AE001354, GB:AE001273, NID:g3329280, PIDN:AAC68416.1, PID:g332928
C)Genetics: Source: serotype D, strain UW-3/Cx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable transport permease - Chlamydia trachomatis (serotype D, strain UW3/Cx) C.Species: Chlamydia trachomatis (c.Species: Chlamydia trachomatis (c.Species: 13-Sep-1998 #text_change 08-Oct-1999 (c.Spate: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999 (c.Spate: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999 (c.Spate) (c.S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 AFVGCAVVFGCFSAAAMLAR-----RREYLYLGGLLSSGVSLLFWLHFASSIFGGSMA 175
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                                                                                                                                                                                                                                                                             113 AFGSAAVIFGLSAAYGAFTKSDLTQIHRILMLALIGLMV--ISLGF---LVVSLFTPMPL 167
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70 MACMG-----SMVWLLSAPPYQEQKRVALLMAAALFEGASIGPLIEL-GINFDPSIVFG 122
                                                    123 AFVGCAVVFGCFSAAAMLAR,-----RREYLYLGGLLSSGVSLLFWLHFASSIFGGSMA 175
                                                                                                                                                                                                                                                                                                                                                                                       176 VFKPBLYFGLLVFVGYIVFDTQEIIEKAHL----GDMDY----VKHALTLFTDFGAVFVRI 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 YDSLKNFRQISPLVQTHLKQVY------LTLCCALVASAAGAY--LHILWNIGGLLTT 69
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10.1%; Score 128.5; DB 2; Length 238;
Best Local Similarity 25.9%; Pred. No. 0.00028;
Matches 63; Conservative 38; Mismatches 95; Indels 47;
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C;Superfamily: Bscherichia coli ybhi protein
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GenCore version 5.1.5
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OM protein - protein search, using sw model

Run on:

May 25, 2003, 11:26:54; Search time 36 Seconds (without alignments) 285.726 Million cell updates/sec

US-09-955-526-4 1272 1 MEGFTSFFDSQSASRNRWSY......LIMLKNASEKEEKKKKRRN 248 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		,	ar		P55061 homo sapien	Q9ia79 paralichthy	P55062 rattus norv	Q9vsh3 drosophila	Q9h3k2 homo sapien			chlamydia	chlamydia			Q9piq8 campylobact						P44477 haemophilus		Q9ksal vibrio chol	O25578 helicobacte		heli	rickettsi	candida a	P27611 bacillus fi		lactoc	Q9alb9 streptococc	48994	72060
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Q9a2a3 caulobacter 047479 loligo blee Q9cdm7 lacrococcus 029470 archaeoglob 09evn4 pseudomonas 051489 borrealia bu P47562 mycoplasma P28008 staphylococ Q95919 polypterus P19845 pseudomonas P45064 haemophilus Q18864 caenorhabdi
YOG3 CAUCR NULM_LOLBL UPK_LACLA Y788 AACTA RNFD_PSEST RNFD_PSEST Y339 BORBU Y320 MYCGE PTMB_STACA NUGM_POLOR NOSY PSEST FTSW HAEIN SUR4_CABEL
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ALIGNMENTS

PRT; 247 AA.	16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update)	ist ammotation update/ (AtBI-1).	IA3.7. mice car grees)	ouse-car cress). 3; Streptophyta, Embryophyta; Tracheophyta;	obyta; eudicotyledons; core éudicots; Rosidae; : Rraceicaceae, brahidoneie	o, brassicactar, Atabidopsis.			1=10618494;	Kawai M., Pan L., Reed J.C., Uchimiya H.; "Evolutionally concerved nlant homologie of the Bay inhihitor," (PI.1)	ell death in yeast.";	. (666		SUE=Leaf;	1=10758491;		"Atb1-1, a plant nomblogue of bax innibitor-1, suppresses bax-induced cell death in yeast and is rapidly uprequlated during wounding and					Asamizu E., Sato S., Nakamura Y., Kotani H.,	9000044	cmailama cmicmosome 3. Al Bank/DDBJ databases.	OF APOPTOSIS.	SUBCELLULAR LOCATION: Integral membrane protein (Potential).	ANTIL: DEDONGS TO THE DIT PARTY.	uced through a collaboratio	cure of bioinformatics and the Embh outstation - ics Institute. There are no restrictions on its	5	ent is not removed. Usage by and for commercial	s a license agreement (See http://www.isb-sib.ch/announce/	MAGGERD-SID.CII).	2;		inhbrri	1.
STANDARD;	(Rel. 40, C) (Rel. 40, La	r-1 (BI-1)	47120 OR K1	iridiplantae	a; Magnolion Braceicales	702;		n N.A.	5876; PubMec	L., Reed	of suppress	54:143-147(]	N.P.	olumbia; TIS	1035; PubMec	le Torres Za	lant nombio	llenge.";	393-399 (2000	N.A.	olumbia,		nalwaia of	7R-1999) to	FUNCTION: SUPPRESSOR	AR LOCATION	Spronge : I	NOT entry is	Swiss insti Bioinformat	profit ins	this statem	ires a lice	ומדד רס דדכי	7; BAA89541	24; AAG35727.1	2002199: Bax	7. TIDEOOR.
ARATH BI1_ARATH O9LD45;	16-OCT-2001 16-OCT-2001 15-JTM-2002	Bax inhibiton	BI-1 OR AT5G4	Eukaryota; Vi	Spermatophyta	NCBI TaxiD=37	[1]	STRAIN=CV. CC	MEDLINE=20086876; PubMed=10618494;	Kawai M., Par	gene capable	FEBS Lett. 46	SECUENCE FROM	STRAIN=cv. Columbia; TISSUE=Leaf	MEDLINE=20224035; PubMed=10758491;	Sanchez P., c	cell death ir	pathogen challenge.";	Plant J. 21:3	[3] SEOUENCE FROM N.A.	STRAIN-cv. Columbia;	Ţ,	Tabata S.;	Submitted (APR-1999)	-!- FUNCTION:	-!- SUBCELLUI		This SWISS-PF	the European	use by non-	modified and this statement	entities requires	כני שבוות מוו מו	EMBL; AB025927; BAA89541.2;	EMBL; AF208124; AAG35727.1;	InterPro: IPE	1110, 1110, 1110, 1111,
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Homo sapiens (Human)
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249 AA;
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 Apoptosis;
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SEQUENCE
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STRAIN=cv. Yamahoushi;
STRAIN=cv. Yamahoushi;
STRAIN=200086976; PubMed=10618494;
MEDLINE=200086976; PubMed=10618494;
Kawai M., Pan L., Reed J.C., Uchimiya H.;
Evolutionally conserved plant homologue of the Bax inhibitor-1 (BI-1)
gene capable of suppressing Bax-induced cell death in yeast.";
FEBS Lett. 464.143-147(1999).
-: FUNCTION: SUPPRESSOR OF APOPTOSIS (BY SIMILARITY).
-: SUBCELULAR LOCATION: Integral membrane protein (Potential).
-: TISSUE SPECIFICITY: UBIQUITOUS.
-: SIMILARITY: BELONGS TO THE BII FAMILY.
                                                                                                                                                                                                                                                                              60 WNIGGILTTIGCIGTWIWLLSCPPYEHQXRLSLLFVSAVLEGASVGPLIXVAIDVDPSIL 119
                                                                                                                                                                                                                                                                                                                         121 FGAFVGCAVVFGCFSAAAMLARRREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFE 180
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                                                                                                                                                                                                                                                                                                                                                                                                         180 LYFGLLIFVGYMVVDTQEIIEKAHLGDMDYVKHSLTLFTDFVAVFVRILIIMLKNSADKE 239
                                                                                                                                                                                                                                                             WNIGGLITTMACMGSMVWLLSAPPYQEQKRVALLMAAALFEGASIGPLIELGINFDPSIV 120
                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                    Oryza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Lillopsida, Poales, Poaceae,
Ehrhartoldeae, Oryzeae, Oryza.
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                                                                                                                                      80.5%; Score 1023.5; DB 1; Length 247;
                                                                                                                                                                    24; Indels
                                                                                                        FD3AAEA713363945 CRC64;
                                                                                                                                                   ; Pred. No. 1.3e-69; 31; Mismatches 24
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Bax inhibitor-1 (BI-1) (OSBI-1).
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InterPro.; IPR002199; Bax inhbtrl.
Pfan; PF01027; UPP0005; I.
PROSITE; PS01243; BII; 1.
                                                                                                        27483 MW;
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Transmembrane
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165
193
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173 * 1
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Matches 192; Conserv
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BII_ORYSA
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61 LNIGGMLTWLGCVGSIAWLFSVPVFEERKRFGILLAAALLEGASVGFLIKLAVDFDSSIL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 WNIGGLLTTMACMGSMVWLLSAPPYQEQKRVALLMAAALFEGASIGPLIELGINFDPSIV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 FGAFVGCAVVFGCFSAAMLARRREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 LYFGLLVFVGYIVFDTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILIIMLKNASEK- 239
                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                           1 MEGFISFFDSOSASRNRWSYDSLKNFROISFLVQTHLKOVYLTLCCALVASAAGAYLHIL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ģ
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Mol. Biol. Cell 1:337-346(1998).
-!- FUNCTION: SUPPRESSOR OF APOPTOSIS.
-!- SUBUNIT: INTERACTS WITH BLC2 AND BCL-XL.
-!- SUBCELAULAR LOCATION: Integral membrane protein (Fotential)
                                                                                                                                                                                                                                                         ij
                                                                                                                                                                                                       68.9%; Score 876.5; DB 1; Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Walter L., Marynen P., Szpirer J., Levan G., Guenther E.; "Identification of a novel conserved human gene, TEGT.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BII HUMAN STANDARD; PRT; 237 AA.
PS55061, 014938; 096550, 01-007-1996 (Rel. 34, Created)
15-UTN-2002 (Rel. 41, Last sequence update)
15-UTN-2002 (Rel. 41, Last annotation update)
Bax inhibitor-1 (BI-1) (Testis enhanced gene transcript).
BII OR TEGT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Cowling R.T., Birnboim H.C.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
                                                                        POTENTIAL.
POTENTIAL.
POTENTIAL.
FEAE334173F6D384 CRC64;
                                                                                                                                                                                                                                                            43;
                                                                                                                                                                                                                             ; Pred. No. 1.1e-58; 40; Mismatches 43
  POTENTIAL
                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Testis;
MEDLINE=96015061; PubMed=8530040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARACTERIZATION.
MEDLINE=98325348; PubMed=9660918;
Xu Q., Reed J.C.;
59
85
113
139
171
233
27114 MW;
                                                                                                                                                                                                                                   66.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomics 28:301-304(1995).
                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A novel, conserved gene of the rat that is developmentally regulated in the testis.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 VWLLSAP--PYQEQKRVALLMAAALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 SAAAMLARRREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELYFGLLVFVGYIVF 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 SYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHILWNI--GGLLTTMACMGSM 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Sprague-Dawley; TISSUE=Testis;
MEDLINE=94281747; PubMed=8012111;
Walter L., Dirks B., Rothermel E., Heyens M., Szpirer C., Levan G.,
Guenther E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mamm. Genome 5:216-221(1994).
-!- FUNCTION: SUPPRESSOR OF APOPTOSIS (BY SIMILARITY).
-!- SUBUNIT: INTERACTS WITH BLC2 AND BCL-XL (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- TISSUE SPECIFICITY: HIGHLY ABUNDANT IN TESTIS.
-!- SIMILARITY: BELONGS TO THE BI1 PAMILY.
--- TISSUE SPECIFICITY: HIGHLY ABUNDANT IN TESTIS.
--- SIMILARITY: BELONGS TO THE BIL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.9%; Score 481.5; DB 1; Length 237; 41.3%; Pred. No. 2.7e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        195 DTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILIIMLKNASEKEEKKK 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BIL RAT STANDARD; PRT; 236 AA.
P5562; 064712;
01-007-1996 (Rel. 34, Created)
01-007-1996 (Rel. 34, Last sequence update)
16-007-2001 (Rel. 34, Last annotation update)
Bax inhibitor-1 (BI-1) (Testis enhanced gene transcript).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIQLIEKAENGDKDYVWHSVDLFLDFITIFRKLMVILALNDKDKKKEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                        344181AA386AB9A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53; Mismatches
                                                                                                                                                                                                                                                                                                                                     POTENTIAL
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Pfam; PP01027; UPP0005; I.
PROSITE; PS01243; B11; 1.
                                                                                                                                                                                                                                                                                                                                     50
73
107
133
170
193
26570 MW;
                                                                                                                                                                                                                                      EMBL; AF220548; AAF61067.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95; Conservative
                                                                                                                                                                                                                                                                                                                  Apoptosis; Transmembrane
TRANSMEM 30 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
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                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the RMBL outstation. the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to TEGT."; Same of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 IWLMATPHSHETEQKRLGLLAGFAFLTGVGLGPALEFCIAVNPSILPTAFWGTAMIFTCF 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 SYDSLKNFRQISFLVQTHLKQVYLTLCCALVASAAGAYLHILWNI--GGLLTTMACMGSM 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neoperygii, Taleosstei, Biteleostei, Neoteleostei, Acanthomorpha, Acanthoperygii, Percomorpha, Pleuronectiformes, Pleuronectoidei, Paralichthyidae, Paralichthys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135 SAAAMLARREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELYFGLLVFVGYIVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 VWLLSAPPYQ--EQKRVALLMAAALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 DIQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILIIMLKNASEKEEKKKKR 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lee J., Jeon J., Song Y.;
"Liver CDN from Japanese flounder with similarity to TEC Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases:
-- FUNCTION: SUPPRESSOR OF APOPTOSIS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6567E73A1AD6238E CRC64;
    !- TISSUE SPECIFICITY: HIGHLY ABUNDANT IN TESTIS.
!- SIMILARITY: BELONGS TO THE BI1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -> P (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.9%; Score 481.5; DB 1
42.7%; Pred. No. 2.7e-29;
iive 52; Mismatches 74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probable Bax inhibitor-1 (BI-1).
Paralichthys olivaceus (Flounder).
                                                                                                                                                                                                                                                                                                                InterPro; IPR002199; Bax inhbtrl.
Pfam; PF01027; UPF0005; 1.
PROSITE; PS01243; BI1; 1.
                                                                                                                                                                                                               EMBL; X75861; CAA53472.1; -.
EMBL; AF033095; AAB87479.1; -.
EMBL; BC000916; AAH00916.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26537 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                          Transmembrane
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                                                                                                                                                                                                                                                                           HGNC:11723; TEGT.
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1103
1133
1160
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1169
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187 1
237 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                             Genew; HGNC:
MIM; 600748;
                                                                                                                                                                                                                                                                                                                                                                        Apoptosis; 1
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 ICLMATPHSHETEQKRIGLL-AVAFLTGVGLGPALELCIAINPSILPTAFMGTAMIFTCF 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 SAAAMLARRREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELYFGLLVFVGYIVF 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Skaryotes, Metazoa, Arthropoda; Mandibulata, Pancrustacea, Hexapoda,
Insecta, Pterygota, Neoptera: Endoprerygota, Diptera, Brachycera,
Muscomorpha; Ephydroidea, Drosophilidae, Prosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 SYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHILWNI--GGLLTTMACMGSM 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 VWLLSAPPYQ--BOKRVALLMAAALFEGASIGPLIBLGINFDPSIVFGAFVGCAVVFGCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 37.7%; Score 479; DB 1; Length 236
Best Local Similarity 43.1%; Pred. No. 4.2e-29;
Matches 100; Conservative 52; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FFA412EC1DC87537 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable Bax inhibitor-1 (BI-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                245 AA
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Pfam; PF01027; UPF0005; I.
PROSITE; PS01243; BI1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26358 MW;
                                                                                                                                                                                                                                                                            EMBL; X75855; CAA53470.1; -.
EMBL; X75856; CAA53471.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Apoptosis; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139
166
206
236 AA;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                       EMBL; X75856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DROME
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Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Ade de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., R. Durbin K.J., Evangelista C.C., Ferraz C., Ferriara S., Fleischmann W., R. Glock A., Gong F., Gorg N., Galbart W.M., Glasser K., Allock A., Gong F., Gorg N.S., Gelbart W.M., Glasser K., Allock A., Gong F., Garrell J.H., Gu.Z., Guan P., Harris M., Allock A., Gong F., Karpen G.H., Re Z., Kennison P., Hauris M., Allock J., Karpen G.H., Re Z., Kennison J.A., Kethum K.A., Hostin D., Houston K.A., Howland T.J., Mernandez J.R., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., Lu X., Markillow G., Milshina N.V., Mobarry C., Morris J., Morris J., Maleon D.L., R. Murlby B., Murphy B., Murphy D., Morris J., Moleon D.L., R. Mount S.M., Moy M., Murphy B., Murphy L., Murshy D.M., Nelson M., Shelen H., Raington K., Sanders R.D.C., Scheeler F., Shen H., Rhenngton K., Sanders R.D.C., Scheeler F., Shen H., Raing X., Massarman D.A., Weinscok G.M., Weissenbach J., Wang X., Walliams S.M., Woodage T., Worley K.C., Mu D., Yang S., Sheng X., Rubing G., Zhan M., Zhang G., Zhang G., Zhang G., Zhang S., Sheng S., Sheng X., Sheng X., Rubing S., Nang S., Sheng X., Rubing S., Nang S., Sheng X., Rubing S., Nang S., Sheng X., Sheng X., Rubing G., Zhang M., Venter J.C., Siden S., Sheng X., Sheng X., Rubing G., Zhang S., Zhong W., Sheng X., Sheng X., Rubing G., Zhang G., Zhang G., Zhang G., Zhang G., Zhang G., Zhang S., Sheng X., Sheng X., Rubing S., Nang S., Sheng X., Rubing S., Rubing S., Sheng X., Rubing S., Rubing S., Sheng X., Rubing S., Rubing S., Sheng X., Ru
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InterPro: JRR002199, Bax inhbtrl.
Pfam, PF01027, UPP0005, I.
PROSITE, PS01243, BI1; 1.
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76
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27574 MW;
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Best Local Similarity 34.44
Matches 77; Conservative
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TRANSMEM 31 51
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                                             GHIT HUMAN STANDARD; PRI; 345 AA.
99H3Z; 09SB94, O9H0P2;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Growth hormone inducible transmembrane protein (Dermal papilla derived
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21154917; PubWed=11230166; Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S., Wiemann S., Weil B., Wellenreuther R., Bauersachs S., Blum H., Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H., Mushor J., Duesterhoeft A., Beyer A., Koehrer K., Strack N., Mewes H.-W., Ottenwaelder B., Obermaler B., Tampe J., Heubner D., Wambutt R., Korn B., Klein M., Poustka A.; Tampe J., Heubner D., Thowards a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs.";
                                                                                                                                           Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
MCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE=Urinary bladder;
Strausberg R.,
Submitted (UU.-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SUBLEARITY: BELONGS TO THE B11 FAMILY.
                                                                                                                                                                                                                   TISSUE-Dermal papilla, Itseda A., Yamashita M., Yoshimoto M.; Mamashita M., Yoshimoto M.; Wolecular cloning of a dermal papilla derived gene."; submitted (DEC-1997) to the EMBL/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                          Mao Y.M., Xie Y., Mu Z.M., Li Y., Huang Y.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR002199; Bax inhbtr1.
Pfam; PF01027; UPF0005; 1.
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EMBL, AF111820; AAD20052.1; -..
EMBL, AF060923; AAG43135.1; -..
EMBL, AL136713; CAB66648.1; -..
EMBL, BC010354; AAH10354.1; -..
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SEQUENCE FROM N.A.
Mei G., Yu W., Gibbs R.
Submitted (FEB-1999) to
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GHIT HUMAN
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Tamura F., Nishimura S., Ohki M.;
Tamura F., Nishimura S., Ohki M.;
Tame B. coli divB mutation, which differentially inhibits synthesis
of certain proteins, is in tRNASerl.";
EMBO J. 3:1103-1107(1984).
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SEQUENCE FROM N.A.
MEDILINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 345;
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                                                                                           13.0%; Score 165; DB 1; 26.3%; Pred. No. 1.4e-05; trive 47; Mismatches 86;
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16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein yccA.
POTENTIAL. POTENTIAL.
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01-APR-1988 (Rel. 07, Last seq.
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61; Conservative
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297 AA;
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                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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STRAIN=S288C / FY1679;
STRAIN=S9132031, PubMed=8553702;
Maurer K.C.T., Urbanus J.H.M., Planta R.J.;
"Sequence analysis of a 30 kb DNA segment from yeast chromosome XIV
SIMILARITY: BELONGS TO THE BIL FAMILY. STRONG, TO H.INFLUENZAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 SASRNRWSYDSLKNFRQISPLVQTH--LKQVY--LTLCCALVASAAGAYLHILWNIGGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 SSSHDRTS------LLSTHKVLRNTYFLLSLTLAFSAITATASTVLMLPSPGLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 TIMACMGSMVWLLSAPPYQ-EQKRVALLMAAAL--FEGASIGPLIELGINFD-PSIVFGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 GSMAVFKFELYFGLLVFVGYIVFDTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILII
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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01-FEB-1996 (Rel. 33, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Hypothetical 33.6 kDa protein in MCK1-RPS19B intergenic region.
YNL305C OR N0405.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77; Indels
                                                                                                                                                                                                                                                                                                                                                                Complete proteome.
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27.0%; Pred. No. 3.4e-05;
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PIR; S07180; S07180.
EcoGene; Ed11113; yccA.
InterPro; IPR002199; Bax inhbtr1.
Pfam; PF01027; UPF0005; I.
PROSITE; PS01243; B11; 1.
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EMBL; AE000199; AAC74056.1; -.
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                                                                                                                                                                                                                                                                                                                                                                  protein;
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158
196
219 AA;
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P48558;
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STRAIN=MADD / Nigg;
MEDLINE=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
carrying a ribosomal protein gene cluster, the genes encoding a plasma membrane protein and a subunit of replication factor C, and novel putative serine/threonine protein kinase gene.";
Yeast 11:1303-1310(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 PLV-QTHLKQVYLTLCCALVASAAGAY------LHI-LWNIGGLLTTMACMGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 -IWLAVSPRPEDYEASVPEPLLTGSSEEPAQEQRRLPWYVLSSYKQKLTLLSIFTLSEAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 SIGPLIELGINFDPSIVFGAFVGCAVVFGCFSAAAMLARREYLYLGGLLSSGVSLLFWL
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=83560;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein TC0206.
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POTENTIAL.
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EMBL; Z71581; CAA595233.1; -.
CAGD; S0005249; YNL305C.
InterPro; IPR00199; Bax inhbtr1.
Pfam; PF01027; UPF0005; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 VFKFELYFGLLVFVGYIVFDTQEIIEKAHL----GDMDY----VKHALTLFTDFGAVFVRI 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 LYLLICYLGELIFVGLIVVDAQSIRRVARSVGDHGDLSYKLSLIMALQMYCNVIMIFWYL 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 MACMG-----SMVWLLSAPPYQEQKRVALLMAAALFEGASIGPLIEL-GINFDPSIVFG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 FATLGVSFYIQAQIQKLSVPAV----MGLFLAYSILEGMFFGTLVPVYAAQFGGGVVWA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 YD--RDYAQDSRLPGTFSSRVYGWMTAGLAVTALTSLGLYATGAYRALFPMW----WIWC 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 YDSLKNFRQISPLVQTHLKQVY-----LTLCCALVASAAGAY--LHILWNIGGLLTT 69
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MEDLINE=21145866; PubMed=11248100;
MEDLINE=21145866; PubMed=11248100;
MEDLINE=27145866; PubMed=11248100;
"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
                               "Genome sequence of an obligate intracellular pathogen of humans:
Chlamydia trachomatis.";
                                                              Chlamydia trachomatis.";
Science 282:778(1998)
-i- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-i- SIMILARITY: BELONGS TO THE BII FAMILY.
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Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.1%; Score 128.5; DB 1; Length 238; 25.9%; Pred. No. 0.0052; Live 38; Mismatches 95; Indels 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FD101F7B3867B8E5 CRC64;
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InterPro. 1PR002199; Bax inhbbrl.
Pfam, PF01027; UPF0005; I.
Hypothetical protein; Transmembran
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26264 MW,
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16-0CT-2001 (Rel. 40, Last seq
16-0CT-2001 (Rel. 40, Last and
Hypothetical protein PM0402.
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hes 63; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 MACMG-----SMVWLLSAPPYQEQKRVALLMAAALFEGASIGPLIEL-GINFDPSIVFG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 FATLGVSFYIQAQIQKLSVPAV----MGLFLAYSVLEGMFFGTMVPVYAAQFGGGIVWA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 AFVGCAVVFGCFSAAAMLAR-----RREYLYLGGLLSSGVSLLFWLHFASSIFGGSMA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 VFKFELYFGLLVFVGYIVFDTQEIIEKAHL----GDMDY----VKHALTLFTDFGAVFVRI
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg
Eisen J., Fraser C.M.;
                                                                                                                    Nucleic Acids Res. 28:1397-1406(2000).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE BI1 FAMILY.
                                                  "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.3%; Score 130.5; DB 1; Length 238; 27.2%; Pred. No. 0.0037; Live 35; Mismatches 95; Indels 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical protein CT819.
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Transmembrane; Cc
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TIGR: TC0206: -.
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TRANSMEM 22 42
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166
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238 AA;
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                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FNBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                87 EQKRVALLMAAAL--FEGASIGPLIBLGINFDP-SIVFGAFVG-CAVVFGCFSAAAMLAR 142
                                                                                                                                                                                                                                                                                                                                                                                                                                143 RREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELYFGLLVFVGYIVFDTQEIIEK 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 KKDMSFLSGTIFALFIVLLLGMVASFFFQSPMLYIAISGLFVVFSTLG-ILYETSNII-- 184
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                     32 IVQTH--LKQVYLTLCCALVASAAGAYLHILWNI--GGLLTTMACMGSMVWLLSAPPYQ- 86
                                                                                                                                                                                                                                                                                                                                                         14 LLNTHKVLRNTYFLLGLTLAFSAVVAYISMSLNLPRPGLILMLAGFYGLLFL----TYKL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20036896; PubMed=10567266; Mickey E.K., Peterson J.D., white O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Raft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamethevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Solence 286:1571-1577(1999).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
SUBCELLULAR LOCATION: Integral membrane protein (Potential). SIMILARITY: BELONGS TO THE BIL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                                                      DB 1; Length 220;
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                                                                                                                                                                                                                                                                             Score 125.5; DB 1; Luc.
Pred. No. 0.0081;
                                                                                                                                                                   Complete proteome
                                                                                                                                                                                                                                                                8EEC2E3FB4B5CDD5 CRC64;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231 AA
                                                                                                                                                                                                                                                                                                            44; Mismatches
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                                                                                                                                                                  Transmembrane;
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                                                                                                                              EMBL, AE006076; AAX02486.1; -.
InterPro; IPR002199; Bax inhbtrl.
Pfam; PF01027; UPF0005; 1.
                                                                                                                                                                                                                                                                23936 MW;
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70
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TRANSMEM 25 4
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220 AA;
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Best Local Similarity
Matches 53; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 MLAQLALVFVLS----MFAQRLSAAVAGALFVGYAALTGLTFSALLFAYSPAAVITAFAV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 CAVVFGCFSAAAMLARR-----REYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFE 180
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MEDIATR=20150912; PubMed=10688204;
MEDIATR=20150912; PubMed=10688204;
MEDIATR=20150912; PubMed=10688204;
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S., Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W., Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M., Whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 LKNFRQISPLVQTHLKQV-----YLTLCCALVASAAGAYL-----HILWNIGGL-LTT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VKSMQÓIAMTQÓKTLDÓVRTFMARTÝSWMAAGLALTÁGVÁYLTAQNEGLAMQVASLRLPL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Campylobacter jejuni.
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 LYFGLLVFVGYIVFDTQEIIEKAHLG-----DMDYVKHALTLFTDFGAVFVRILII 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- SUBCELIULAR LOCATION: Integral membrane protein (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 124; DB 1; Length 231;
Pred. No. 0.011;
1; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                Transmembrane; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24447 MW; BBB7D76A6445D9C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Pred. No. 0.01.
41; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
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                                                                                                                                                                                                                                                                                                                 InterPro, IPR002199; Bax inhbtrl.
Pfam; PF01027; UPF0005; I.
                                                                                                                                                                                                                                                  EMBL; AE001942; AAF10471.1; -.
TIGR; DR0893; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein Cj0236c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 26.2 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 403:665-668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Campylobacter.
NCBI_TaxID=197;
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Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito. Mori H.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 SMVWLLSAPPYQEQKRVALLMAAALF----EGASIGPLI--ELGINFDPSIVFGAFVGC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 AVVFGCFSAAAMLARREYLYLGG-----LLSSGVSLLFWLHFASSIFGGSMAVFKFELY 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 TVAFAGLSVFAM-NTKKDFTVMGKALFIVLIVIVAASLINLFFQSSIVNLAISA---- 178
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           8 YSRSKEFENTRSSELSIFIKÖTYQLFAASLLAATVGAYVGIFALASFFIQSQVTFWILFA 67
                                                                                                                                                                                                                                                                                                                                                                                                           20 YDSLKNFRQI-SPLVQTHLKQVYLTLCCALVASAAGAYLHIL----WNIGGLLTTWACMG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                            31;
                                                                                                                                                                                                                                                                                                                                      9.7%; Score 123.5; DB 1; Length 231; 26.8%; Pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 FGLLVFVGYIVFDTQEIIEKAHLGDMDY-VKHALTLFTDFGAVFVRILIIM 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                       Pred. No. 0.012;
38; Mismatches 100; Indels
                                                                                                                                                                                                Transmembrane, Complete proteome POTENTIAL.
                                                                                                                                                                                                                                                                                  POTENTIAL.
279E67CA380336C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1998 (Rel' 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein ybhi.
                                                                                                                                                                                                                                 POTENTIAL. POTENTIAL.
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                                                                                                                           EMBL, AL139074, CAB72705.1, ...
InterPro; IPR002199, Bax inhbtr1.
Pfam, PF01027; UPF0005; I.
Pypothetical protein, Transmembrar TRANSMEM
                                                                                                                                                                                                               56 PO
78 PO
103 PO
163 PO
190 PO
25487 MW;
                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                     231 AA;
                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=562;
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                                                                                                                                                                                                                                                                                                                                                                          62;
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ID YBHL_ECOLI
AC P75768;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 YGYTTKRDLSGFGNMLFMALIGIVLASLVN--FWLK-----SEALMWAVTYIGVIVF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 VWLLSAPPYQEQKRVALLMAAALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCFSA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 AAMLARR----REYLY---LGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELYFGLLVF 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 VQTHLKQVY-----LTLCCALVASAAGAYLHILWN----IGGLLTTMA---CMGSM 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 LQTYMAQVYGWMTVGLLLTAFVAWYAANSAAVMELLFTNRVFLIGLIIAQLALVIVLSAM 76
"A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map."; DNA Res. 3:137-155(1996).
-1- SUBCELLUIAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 VGLTAYDTQKLKNMGEQIDTRDISNLRKYSILGALTLYLDFINLFLMLLRI 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189 VGYIVFDTQEII----EKAHLGDMDYVKH-----ALTLFTDFGAVFVRILII 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 122; DB 1; Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81; Indels
                                                                                                                                                                                                                                                                                                                     Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                    7A59105563D5DFC8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.6%; Score 122,
25.5%; Pred. No. 0.016;
tive 41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                       Transmembrane;
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Job time : 39 secs
                                                                                                                                                                                                                                                EMBL, D90716, BAA3544.1; -. GroGens, EG1368, Ybh.. InterPro; IPR001199; Bax inbbr1. Pfam; PF01027; UPF0005, I.
                                                                                                                                                                                                                                                                                                                                                                   100
123
157
184
227
25902 MW,
                                                                                                                                                                                                                                    EMBL; AE000181; AAC73873.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59; Conservative
                                                                                                                                                                                                                                                                                                                     Hypothetical protein;
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137
164
207
234 AA;
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TRANSMEM
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May 25, 2003, 12:05:29; Search time 58 Seconds (without alignments) 881.029 Million cell updates/sec
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                                                                                                                                                                                                                                         US-09-955-526-4
1272
1 MEGFISFFDSQSASRNRWSY......LIIMLKNASEKEEKKKKRRN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      671580
GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                 671580 segs, 206047115 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                              OM protein - protein search, using sw model
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1: Sp_archea:*
2: Sp_bacteria:*
3: Sp_Lungi:*
4: Sp_lungi:*
5: Sp_inwertebrate:*
6: Sp_mammal:*
7: Sp_mhc:*
7: Sp_nhc:*
8: Sp_organelle:*
9: Sp_phage:*
10: Sp_organelle:*
11: Sp_organelle:*
12: Sp_virus:*
13: Sp_virus:*
14: Sp_unclassified:*
15: Sp_virus:*
16: Sp_bacteriap:*
17: Sp_archerate:*
18: Sp_virus:*
18: Sp_virus:*
19: Sp_virus:*
11: Sp_virus:*
11: Sp_virus:*
12: Sp_virus:*
13: Sp_virus:*
14: Sp_niclassified:*
15: Sp_virus:*
16: Sp_bacteriap:*
17: Sp_archeap:*
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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Description	Q93xb9 nicotiana t Q93xc0 brassica na	Q8w196 brassica ol 093x12 hordeum wil	Q9d2c7 mus musculu	O23599 arabidopsis	Q9ltb6 arabidopsis	Q9vib2 drosophila	Q8t8z4 drosophila	Q8zg61 salmonella	Q9vz34 drosophila	Q91vc9 mus musculu	Q8z7r5 salmonella	Q95309 sús scrofa	Q8xd81 escherichia	08y034 ralstonia s
SUMMARIES	Q93XB9 Q93XC0	Q8W196 Q93XL2	Q9D2C7	023599	Q9LTB6	Q9VIB2	Q8T8Z4	Q8ZQ61	Q9VZ34	Q91VC9	Q8Z7R5	095309	QBXD81	Q8Y034
DB	33	10	H	10	10	Ŋ	Ŋ	16	'n	11	16	9	16	16
% Query Match Length DB	249	246	237	262	187	305	365	219	341	346	219	99	219	233
% Query Match	89.2	78.8	38.6	37.1	34.2	15.1	15.1	13.7	13.5	13.4	13.4	12.9	12.4	11.8
Score	1134.5	1002.5	490.5	472	435.5	192	192	174.5	172	171	170.5	164	157.5	150
Result No.	7 7 7	W 4	'n	9	7	80	თ	10	11	12	13	14	15	16

074888 schizosacch	P91373 caenorhabdi	Q8v310 camelpox vi	Q8qq86 camelpox vi	Q8yel9 brucella me		Q8qrt8 chimpanzee	Q8zgwl yersinia pe	Q9mlv9 arabidopsis	Q95t37 drosophila	Q9v6h7 drosophila	Q8x804 escherichia	Q9hc19 homo sapien	Q9v6h6 drosophila	Q92161 rhizobium m	Q8t8w2 drosophila	Q94gn3 oryza sativ				Q8zkw9 salmonella	Q8uc16 agrobacteri		Q8tam3 homo sapien	Q9atp8 acetabulari		σ	Ы	Q8y6el listeria mo	
074888	P91373	: Q8V310	980080	CBYEL9	Q9Y6G2														Q94A20			Q969X1	QBTAM3				Q9VFM3		
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266	342	237	237	245	319	228	236	239	316	324	234	284	239	245	244	229	210	232	256	232	260	311	311	1107	1112	234	264	629	
11.3	11.3	11.1	11.1	10.7	10.4	10.3	10.1	9.8	7.6	9.7	9.6	9.4	ю Э.Э		•	•	6.8		8.8							8.3		•	
144	143.5	141.5	141.5	136.5	132	131.5	128	124.5	123	123	122	119	118.5	117.5	116	113.5	113	112	112	111	109	109	109	108.5	\circ	106	106	106	
17	18	. 19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

RESULT 1

80 80 0 80 80 0	DEC-2001 (TERMELE). 19, Creat	; 249 AA. ed) sequence update)
585	01-MAK-2002 (Trembirel. 20, Last Bax inhibitor 1. BI-1.	annotation update)
800	Nicotiana tabacum (Common Eukaryota;	tobacco). Streptophyta; Embryophyta; Tracheophyta;
SSS	Spermatophyta; Magnoliophy Asteridae; euasterids I; S MCDI maxid-1007.	ledons; core eudicots; lanaceae; Nicotiana.
5 Z G		
R.	STRAIN=CV. SR-1; TISS	
E E		:: :::::::::::::::::::::::::::::::::::
목肾	Submitted (JUN-2001)	how wicociana cabacamo, , nk/DDBJ databases.
R I		
전 전 전 1	OR InterPro; IPR002199; Bax_inhbtrl.	
4 E		
S S	PROSITE; PS00225; CRYSTALLIN BE SEQUENCE 249 AA; 27604 MW;	TAGAMMA; UNKNOWN_1. 776ECC35BEBFB9F8 CRC64;
ÓΜ̈́ Ẍ́	Query Match 89.2%; Score 1134.5; DB Best Local Similarity 87.1%; Pred. No. 5.7e-92; Matches 21; Mismatches 10	1.5; DB 10; Length 249; 5.7e-92; Thes 10; Indels 1; Gaps
ò	1 MEGFTSFFDSOSA-SRNRWSYD	VQTHLKQVYLTLCCALVASAAGAYLHI 59
Op	DE 1 MESCTSFFNSQSASSRNRWSYDSLKNFRQISPFVQTHLKKVVLSLCCALVASAAGAYLHI	VQTHLKKVYLSLCCALVASAAGAYLHI 60
ò	9	LLMAAALFEGASIGPLIELGINFDPSI 119
g	0b 61 LWNIGGLLTTLGCVGSIVWLMATPLYEEQKRIALLMAAALFKGASIGPLIBLAIDFDPSI	LIMAAALFKGASIGPLIBLAIDFDPSI 120

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PRELIMINARY;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
247
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240 DKKKRRRN
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                                                                           RESULT 3
Q8W196
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                                                                                                                                                       240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brassica napus (Rape), and
Brassica oleracea (Cauliflower).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; Rosidae;
eurosids II, Brassicales; Brassicaceae, Brassica.
NCBI_TaxID=3708, 3712;
                                                                                                    180 ELYFGLLVFVGYIVFDTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILIIMLKNASEK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SPECIES-B.O.Cleracea.
Coupe S.A., Sinclair B.K., Watson L.M., Bucknell T.T., Eason J.R.;
"The isolation and characterization of broccoli homologs to
Arabidopsis PCD genes, LSDI and BI: their role during cell death and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MDSFSSFFDSQPGSRS-WSYDSLKNLRQISPSVQNHLKRVYLTLCCALVASAFGAYLHVL
VFGAFVGCAVVFGCFSAAAMLARREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKF
                         79.4%; Score 1010.5; DB 10; Length 247; 75.4%; Pred. No. 4.5e-81; ive 35; Mismatches 25; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bolduc N., Brisson L.; "Characterization of Bax inhibitor 1 from Brassica napus."; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Senescence...;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AFF30555; AAK73101.1; -.
EMBL; AFF3052320; AAK75079.1; -.
InterPro; IPR002199; Bax inhbtr1.
InterPro; IPR001064; CYYStallin.
Pfam. PF010.27; UPF000.5; 1.
PROSITE; PS01243; B11; UNKNOWN 1.
PROSITE; PS01243; B11; UNKNOWN 1.
SEOUENCE 247 AA; 27526 MW; FSA5B5EFF6D4E8DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 20, Last annotation update)
Bax inhibitor 1 (Bax inhibitor-like protein).
BI-1 OR BII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SPECIES=B.napus; STRAIN=CV. WESTAR; TISSUE=LEAF;
                                                                                                                                                                                                                                                                                                                                                                                            247 AA
                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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Matches 187, Conservative
                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                            248
                                                                                                                                                                                                                                                         241 EEKKKKRRN 249
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     120
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61 WNIGGLITTMACMGSWVWLLSAPPYQEQKRVALLMAAALFEGASIGPLIELGINFDPSIV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 WNIGGILTTIACCGTWIWLLSCPPYEQQKRLSLLFLSAVLEGASVGPLIKVAVDPDFSIL 119
                                                                                                                                                                                                                                    Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II, Brassicales, Brassicaceae, Brassica.
NCBL_TAXID=3712,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MEGFTSFFDSQSASRNRWSYDSLKNFRQISPLVQTHIKQVYLTLCCALVASAAGAYLHIL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MESFSSFFDSQPGSRS-WSYESLKNIHQISPSVQNHLKRVYLTLCCALVASAFGAYLHVL 59
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lilliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                              Coupe S.A., Sinclair B.K., Watson L.M., Bucknell T.T., Eason J.R., "The isolation and characterization of broccoli homologs to Arabidopsis FCD genes, LSD1 and B1: their role during cell death an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 LYFGLLVFVGYIVFDTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILLIMLKNASEKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     senescence.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF453321; AAL50980.1; -
InterPro; IPR001299; Bax inhbcr1.
InterPro; IPR001064; Crystallin.
Pfan; PF01027; UPF0005; 1.
PR0SITE; PS01243; B11; UNKNOWN 1.
PROSITE; PS00225; CRYSTALLIN BETACAMA; UNKNOWN 1.
SEQUENCE 246 AA; 27375 MW; EBD0A01421B2DA2E CRC64;
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Last annotation update)
                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78.8%; Score 1002.5; DB 176.0%; Pred. No. 2.2e-80; iive 33; Mismatches 25;
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                                                             Created)
PRT;
                                                                                                                                                                                                          Brassica oleracea (Cauliflower).
                                                      01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                Bax inhibitor-like protein
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Matches 187; Conservative
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Matches
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SECURINE FROM N.A.

KAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Arawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Betalov S., Casavant T.,

Ruchl P., Lewis S., Matsuo Y., Nikalio I., Pesole G., Quackenbush J.,

Kuehl P., Lewis S., Matsuo Y., Nikalio I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fulita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Narchionni L., Mashima J., Monzarelli J., Mombaerts P.,

Lyons P., Narchionni L., Mashima J., Mazarelli J., Mombaerts P.,

Assaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Huckelhoven R., Dechert C., Trujillo M., Kogel K.H.;
Huckelhoven R., Dechert C., Trujillo M., Kogel K.H.;
"Expression analysis of putative cell death regulator genes in near-
isogenic, resistent and susceptible barley lines inoculated with the
powdery mildew fungus.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ290421; CAC37797.1; -.
InterPro; IPR002199; Bax_inhbr1.
Pfam; PF01027; UPF0005; 1.
SEQUENCE 247 AA; 26962 MM; 4DBDEPIEFAE22CC4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SFFDSQSASRNRWSYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHILWNIGG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 AFYSTSSAAASGWGHDSLKNFRQISPAVQSHLKLVYLTLCFALASSAVGAYLHIALNIGG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 GTAIAFGCFSGAAIIAKRREYLYLGGLLSSGLSILLWLOFVTSIFGHSSGSFMFEVYFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 GCAVVFGCFSAAAMLARREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELYFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                           Length 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            42; Indels
                           Hueckelhoven R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9D2C7;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
5031406905Rik protein (RIKEN CDNA 5031406P05 gene).
                                                                                                                                                                                                                                                                                                                                                                                                        69.4%; Score 883; DB 10; 67.8%; Pred. No. 7.1e-70; cive 36; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
STRAIN=CV. PALLAS; TISSUE=LEAF;
                                                                                                  SEQUENCE FROM N.A.
STRAIN=CV. PALLAS; TISSUE=LEAF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 164; Conservative
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Best Local
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SEQUENCE FROM N.A.

MEDLINE=99121113; PubMed=9461215;

MEDLINE=99121113; PubMed=9461215;

MEDLINE=99121113; PubMed=9461215;

BergAmp R., Dirkse W., van Staveren M., Stiekema W., Drost L.,

BergAmp R., Dirkse W. van Staveren M., Stiekema W., Drost L.,

Ridley P., Hudgon S.A., Patel K., Murphy G., Piffanelli P., Wedler H.,

Ridley P., Hudgon S.A., Patel K., Murphy G., Pohl T.M., Terryn N.,

Andler E., Wandhutt R., De Clerck R., van Montagu M., Lecharny A.,

Auborg S., Gy I., Kreis M., Lao N., Kavanagh T., Hempel S., Kotter P.,

Raborg S., Gy I., Kreis M., Pank B., Mueller-Auer S.,

Silvey M., James R., Montfort A., Pons A., Pujddomenech P., Douka A.,

Voukelatou B., Milioni D., Hatzopoulos P., Piravandi E., Obermaier B.,

Noukelatou B., Milioni D., Hatzopoulos P., Piravandi E., Obermaier B.,

Palme K., Benes V., Rechman S., Ansorge W., Cooke R., Berger C.,

Palme K., Benes V., Rechman S., Ansorge W., Cooke R., Berger C.,

Belseny M., Voet M., Volckart G., Mewes H.W., Klosterman S.,

Analysis of I.9 Mb of contiguous sequence from chromosome 4 of

Nature 391:485-488(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 SLSALYARRSYLFLGGILMSAMSLML-LSSLGNLFFGSIWLFQANLYLGLLVMCGFVLF 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 VWLLSAPPYQ--EQKRVALLMAAALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 SAAAMLARRREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELYFGLLVFVGYIVF 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 SYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHILWNI--GGLLTTMACMGSM 76
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y., "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.6%; Score 490.5; DB 11; Length 237; 43.1%; Pred. No. 2.1e-35; Live 52; Mismatches 73; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 DIQLIIEKAEHGDKDYIWHCVDLFLDFVTLFRKIMLILAFN--EKDKKKEKK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195 DIQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILIIMLKNASEKEEKKKKR 246
                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AK019865; BAB31892.1; -.
EMBL; EC0055882, ARHOS588.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:1915559; 5031406P05Rik.
InterPro; IPR001399; Bax inhbrr1.
InterPro; IPR001064; Crystallin.
Pfam; PF01027; UPF0005; 1.
PR05TIE; PS01027; UPF0005; 1.
PR05TIE; PS01028; BII, UNKNOWN 1.
PR05TIE; PS01028; CRYSTALLIN BETACAMMA; UNKNOWN 1.
SEQUENCE 237 AA; 26477 NW; 788E6E27EB34AFPC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 29.3 kDa protein (TEGT protein homolog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100; Conservative
                                                                                                                                                                    Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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CG1287 protein.
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                                   RESULT 8
Q9VIB2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0TN-2002 (TrEMBLrel. 15, Last annotation update)
01-JUN-2002 (TrEMBLrel.)
01-JUN-2002 sinhibitor-1.

Arabidopsis thaliana (Mouse-ear cress).

Arabidopsis thaliana (Mouse-ear cress).

Arabidopsis thaliana (Mouse-ear cress).

Spermarophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TAXID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 ITAFLGTAVIFFCFSAVAMLARRREYIYLGGILSSGFSLLTWLKNSDQFAS-----AT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 FKFELYFGLLVFVGYIVFDTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILIIMLKNA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 FGAFVGCAVVFGCFSAAAMLARREYLYLGGLLSSGVSLLFWL----HFASSIFGGSMAV 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 NIGGLLTTMACMGSMV-WLLSAPPYQEQXRVALLMAAALFEGASIGPLIELGINFDPSIV 120
                                                                                                                                                                                                                                                                                         87 EOKRVALLMAAALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCFSAAAMLARRREY 146
                                                                                                                                                                                                                                                                                                                94 EAKRLYLLFLFALLKGASVGPMIMLVIDFDSSVLVTAFVGTAVAFVCFSAAAMLATRREY 153
                                                                                                                                                                                                                                                                                                                                                                       147 LYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELYFGLLVFVGYIVFDTQEIIEKAHLG 206
                                                                                                                                                                                                                                                                                                                                                                                            154 LYHGASLACCMSILWWVQIASSIFGGSTTVVKFELYFGLLIFVGYIVVDTQMITEKAHHG 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Structural analysis of Arabidopsis thaliana chromosome 5. XI."; Submitted (APR-1599) to the EMBL/GenBank/DDBJ databases.
EMBL, AB025609; BAA98108 1; InterPro; IPR002199; Bax inhbtr1.
InterPro; IPR0102199; Bax inhbtr1.
PR01027; UPR0005; I.
PR051TE; PS01243; B1; UNROKON 1.
SEQUENCE 187 A4, 20867 MW; 976978A70592CF1E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=COLUMBIA;
Kaneko I., Katoh I., Asamizu E., Sato S., Nakamura Y., Kotani H.
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                                                                                                                                                                                                           Length 262;
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                                   EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; 297343; CAB10538.2; -.
                                                                                          EMBL; AL161546; CAB78761.1; -.
InterPro; IPR002199; Bax inhbrr1.
Pfam, PF01027; UPF0005; I.
PROSITE; PS01243; B11; UNKNOWN 1.
SEQUENCE 262 AA; 29337 MW; 04111E60CE90F24F CRC64;
                                                                                                                                                                                                              Match 37.1%; Score 472; DB 10; Local Similarity 61.7%; Pred. No. 9.8e-34; es 95; Conservative 22; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.2%; Score 435.5; DB 1 ilarity 50.0%; Pred; No. 1.1e-30; Conservative 32; Mismatches 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 DMDYVQHSFTFFTDFASLFVQILVLNMLIILEKK 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   207 DMDYVKHALTLFTDFGAVFVRILIIMLKNASEKE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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AD-----RIRRN 183
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es 96; Conserv
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                  SEQUENCE FROM N.A.
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Matches
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Q9LTB6
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RX MEDLINE=20196006; PubMed=10731112;
RA Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D. Celniker S.E., Holt R.A., Anburner M., Henderson S.N.,
Button G.G., Mortnan J.R., Yandell M.D., Zhang Q., Chen L.K.,
RA Amanatides R.A., Lewis S.E., Islazel R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Ragers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Addrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Bacnos P.V., Bernan B.P., Bhandari D., Botcharkov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler F.,
RA Borkova D., Botcher A., Deng Z., Mays A.D., Dew I., Dreitz R.M.,
RA Cherry J.M., Cawley S., Dahle C., Davenpoort L. B., Davies P.
RA Cherry J.M., Cawley S., Dahle C., Davenpoort L. B., Davies P.
RA Glodek A., Godpielista C.C., Ferraz C., Perriera S., Fleischmann W.,
RA Glodek A., Godpe F., Gorrell J.H., Bow I., Diez S.M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Marvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Marvey D., Krait C., Kratt C., Kratt S., Kulp D., Lai Z.,
Liu X., Mattei B., McIntosh T.C., McIeod M.P., McRherson D.L.,
RA Harris N.L., Marvis W.A., Mixphy B., Murphy L., Muzny D.M., Nelson D.L.,
Rabon D.R., Woly M., Wurphy B., Murphy L., Muzny D.M., Nelson D.L.,
Rabon D.R., Wolson K.A., Nixon K., Nusskern D.R., Pacte D.W., Palazzolo M., Pittuma G.S., Pan S., Pollard J., Wasserhaboth J.,
Rabon D.R., Wasserman D.A., Weinsechen B., Sun E.,
Spirekas R., Tector C., Thurner R., Venter B., Wang A.H., Wang X.,
Rainswa R., Rander R.W., Rubin G.M., Weissenbach J.,
Rainswa R., Woodage T., Worley K.C., Wu D., Yang S., Zhu K., Smith H.O.,
Rainswa R., Woodage T., Worley K.C., Wu D., Yang S., Zhu K., Smith H.O.,
Rainswa R., Woodage T., Worley K.C., Wu D., Yang S., Zhu K., Smith H.,
Rainswa R., Rainswa R., Rubin G.W., Venter B., Spiresen R.,
Rainswa R., Rai
                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota, Neoptera; Endopterygota, Diptera; Brachycera; Muscomorpha;
Bphydroidea, Drosophilidae; Drosophila.
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                                                                                                                  Last sequence update)
Last annotation update)
305 AA
                                                                          Created)
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                                                                          01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2002 (TrEMBLrel. 21,
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Matches 61; Conservative
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SEQUENCE 305 AA: 3254
PRELIMINARY;
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RESULT 9 Q8T8Z4

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FROM N.A.
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Best Local Similarity 29.6%
Matches 67; Conservative
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Nature
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145 GFGAKQLAWLVHCAVL-GAVLAPMCLLG----GPILTKALLYTSGIVGALSTVAACAPSE 199
                                                                                                                                   Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Tracheara, Hexapoda, Insecta,
Perygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidee, Drosophila.
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                                                                                               145 EYLYLGGLLSSGVSLLF----WLHFASSIFGGSMAVFKFELYFGLLVFVGYIVFDTQ 197
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Gavez C.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Ninoo J., Pacleb J., Paragas V., Park S.
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
Celniker S.,
Submitted (JAN-2012) to the EMBL/GenBank/DDBJ databases.
EMBL, AY075204; AAL68072.1; -
                                                                                                                                                                                                                     198 EIIEKAHLGDM-----DYVKHALTLFTDFGAVFVRILIIMLKNASEKEEKKKKRRN 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
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NCBI_TaxID=602;
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RESULT 10 Q8ZQ61

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XX Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adamstides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Accorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
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MEDLINE=21534948; PubMed=11677609;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.7%; Score 174.5; DB 16
29.6%; Pred. No. 1.1e-07;
tive 42; Mismatches 76;
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SEQUENCE FROM N.A.
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Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
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We J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhang L.,
Schence 2972185-219512000).
Science 2972185-219512000).
Richervo, IPRO02199, Bax inhburi.
Richervo, IPRO02199, Bax inhburi.
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"Identification, isolation, and cloning of growth hormone (GH)-inducible interscapular brown adipose complementary deoxyribonucleic acid from GH antagonist mice.";
Endocrinology 142:2937-2945(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95 MAAALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCFSAAAMLARREYLYLGGLLS 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UTM-2002 (TrEMBLrel. 21, Last annotation update)
Growth hormone-inducible membrane protein (Similar to PTD010 protein)
(Hypothetical 37.3 kDa protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 CVITAAAAATFRSHRLLELASRGGILATIASLALVIGSGAVARSIEYQPGLGAKHLAWA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46 CALVASAAGAYL--HILWNI---GGLLTTMACM-----GSMVWLLSAPPYQEQKRVALL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.5%; Score 172; DB 5; Length 341; 26.5%; Pred. No. 3e-07; tive 46; Mismatches 77; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFGM; PF01027; UPF0005; 1.
SEQUENCE 341 AA; 35817 MW; 7A2AB68A8C6A5525 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             346 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206 ----GDMDYVKHALTLFTDFGAVFVRILIIM 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             304 QYSYTPYDPINASMSIYMDVLNIFIRIVTIL 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
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MEDLINE=21308975; PubMed=11416014;
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es 56; Conserv
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Matches
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Q91VC9
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Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Enker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamiln M., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., "Complete genome sequence of a multiple drug resistant Salmonella enteriors servor Typhi. (T18.")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 VSLLFWLHFASSIFGGSM-----AVFKFELYFGLLVFVGYIVFDTQEIIEKAHLG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97 AALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCFSAAAMLARRREYLYLGGLLSSG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 LTLCCALVASAAGAYLHIL----W-NIGGLLTIMACMGSMVWLLSAPPYQEQKRVALLMA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               32;
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                                                                                                                                                                                                                                                                                                                                                                                                       Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                    13.4%; Score 171; DB 11; Length 3 25.9%; Pred. No. 3.7e-07; tive 47; Mismatches 84; Indels
                                                                                                    Strausberg R.;
Submitted (UTL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF412297, AALO7803.1; -.
EMBL, BC008622, AAH08622.1; -.
EMBL, BC010224, AAH10224.1; -.
Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AL627269, CAD08212.1, -.
InterPro; IPR002199; Bax_inhbtr1.
Pfam; PF01027; UPF0005; I.
PROSITE; PS0124; B11; UNKNOWN_1.
SEQUENCE cal protein; Complete proteome.
SEQUENCE 219 AA; 23347 MW; 914661A809EF6E97 CRC64;
                                                                                                                                                                                                                                        MGD; MGI:1913342; Ghitm.
InterPro; IPR02199; Bax inhbtr1.
Pfam, PR01027; UPF0005; I.
Hypothetical protein.
SEQUENCE 346 AA; 37275 MW; ICFB22B2612BB70D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 DM-----DYVKHALTLFTDFGAVFVRILLIMLKNASEKE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219 AA
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                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 25.9°
Matches 57, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Putative membrane protein
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                                                                            SEQUENCE FROM N.A.
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NCBI_TaxID=601;
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                 11;
                                                                                     83 PPYQ-EQKRVALLMAAAL--FEGASIGPLIELGINFDPSIVFG-AFVGCAVVFGCFSAAA 138
                                                                                                     19 SYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHILMNI--GGLLTTMACMGSM 76
                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 NFDALLKFSHITPSTQQHLKKVYASFALCMFVAAAGAYVHVVTRFIQAGILSALGSLGLM 68
                                                          9 RDRSSLLSTHKVLRNTYFILSLTLAFSAITATASTVLMLPSPGLILTLVGMYGLMFL--- 65
                                       RQISPLVQTH--LKQVY--LTLCCALVASAAGAYLHILWNIGGLLTTMACMGSMVWLLSA 82
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE-SMALL INTESTINE;
Winteroe A.K., Fredholm M., Davies W.;
"Evaluation and characterization of a porcine small intestine CDNA"
                                                                                                                                                   Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                     139 MLARREYLYLGGLLSSGVSLLF------WLHFASSIFGGSMAVFKFELYFGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-UTN-2002 (TrEMBLrel. 21, Last annotation update)
Putative carrier/transport protein.
YCCA OR 21322 OR ECSIO54.
Escherichia coli 0157:H7.
Bacteria, Proteobacteria, gamma subdivision, Enterobacteriaceae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.9%; Score 164; DB 6; Length 99; 36.3%; Pred. No. 4e-07; ive 19; Mismatches 35; Indels
Pred. No. 2.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; Z81159; CAB03546.1; -
InterPro; IPR002199; Bax_inhbtr1.
Pfam; PF01027; UPF0005; 1.
NON_TER
                                                                                                                                                                                                187 VFVGYIVFDTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILIIM 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 99 AA; 10846 MW; EA009C94B5EE6211 CRC64;
                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                 42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 VWLLSAPPYQ--EOKRVALLMAAALFEGASI 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 IWLMATPHSHETEQKRLGLLAGFAFLTGVGL 99
                                                                                                                                                                                                                                                                                              Created)
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                                                                                                                                                                                                                                                                                                         .. 02,
       29.2%;
                                                                                                                                                                                                                                                                                             01-FEB-1997 (TrEMBLrel. 02,
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Best Local Similarity 36.33
Matches 33; Conservative
                   66; Conservative
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                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                 TEGT protein (Fragment)
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NCBI_TaxID=83334;
[1]
       Best Local Similarity
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01-JUN-2002
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095309
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                   Matches
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STRAIN=OLS7:H7 / RIMD 0509952;

XX MEDLINE=21156231; PubMed=11258796;
XM Hayashi T. Makino K., Ohnishi M., Kurokawa K., Ishli K., Yokoyama K., Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishli K., Yokoyama K., Han C.-G., Ohtsubo B., Nakayama K., Murata T., Tanaka M., Tobe T., Kulara S., Shiba T., Hattori M., Shinagawa H., Yasunaga T., Kulara S., Shiba T., Hattori M., Shinagawa H., Yasunaga T., Kulara S., Shiba T., Hattori M., Shinagawa H., Yasunaga T., Kulara S., Shiba T., Hattori M., Shinagawa H., Yasunaga T., Kulara S., Shiba T., Hattori M., Shinagawa H., Yasunaga T., Kulara S., Shiba T., Hattori M., Shinagawa H., Yasunaga T., Kulara S., Shiba T., Hattori M., Shinagawa H., Yasunaga T., Nama S., Shiba S., Shiba H., Shinagawa H., Yasunaga T., Shinagawa H., Yasunaga T., Shinagawa H., Yasunaga T., Hattori M., Yasunaga T., Shinagawa H., Yasunaga T., Shinagawa H., Yasunaga T., Hattori M., Yasunaga T., Shinagawa H., Yasunaga T., Hattori M., Yasunaga T., Hattori M., Yasunaga T., Shinagawa H., Yasunaga T., Yasunaga T., Hattori M., Yasunaga T., Shinagawa H., Yasunaga T., Yasunaga T., Hattori M., Yasunaga T., Hattori M., Yasunaga T., Hattori M., Yasunaga M., Yasunaga T., Hattori M., Yasunaga M., Yasunaga M., Yasunaga M., Yasunaga T., Hattori M., Yasunaga M., Yasunaga M., Yasunaga M., Yasunaga M., Yasunaga M., Yasunaga M., Yasunaga M., Yasunaga M., Yasunaga M., Yasunaga M., Yasunaga M., Yasunaga M., Yasunaga M., Yasunaga M., Yasunaga M., Yasunaga M., Yasunaga M., Yasunaga M., Yasunaga M., Yasunaga M., Yasunaga M., Yasunaga M., Yasunaga M., Yasunaga M., Yasunaga M., Yasunaga M., Yasunaga M., Yasunaga M., Yasun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 VGCAVVFGCFSAAAMLARRREYLYLGGLLSSGVSLLF------WLHFASSIFGG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 TIMACMGSMVWLLSAPPYQEQKRVALLMAAAL--FEGASIGPLIELGINFD-PSIVFGAF 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 SSSHDRTS------LLSTHKVLRNTYPLLSLTLAFSALTATASTVLMLPSPGLI 53
STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III., Burland V., Mau B., Glasner J.D.,
Rose D.J., Maybew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck B.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.,
"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 16; Length 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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12.4%; Score 157.5; DB 16;
Best Local Similarity 26.7%; Pred. No. 3.5e-06;
Matches 64; Conservative 45; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: May 25, 2003, 12:22:52
Job time : 61 secs
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SEQUENCE 219 AA;
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